

# SEQUENCE LISTING

<110> Bristol-Myers Squibb Company

<120> POLYNUCLEOTIDES ENCODING NOVEL HUMAN PHOSPHATASES

<130> D0072.NP

<150> US 60/256,868

<151> 2000-12-20

<150> US 60/280,186

<151> 2001-03-30

<150> US 60/287,735

<151> 2001-05-01

<150> US 60/295,848

<151> 2001-06-05

<150> US 60/300,465

<151> 2001-06-25

<160> 208

<170> PatentIn version 3.0

<210> 1

<211> 144

<212> DNA

<213> HOMO SAPIENS

<400> 1

ctagtttact tctacaattt cggatggaag gattatggtg tagcgtctct tactactatc 60

ctagatatgg tgaaggatgat gacatttgcc ttacaggaag gaaaagtagc tatccattgt 120

catgcagggc ttggtcgaac aggt 144

<210> 2

<211> 48

<212> PRT

<213> HOMO SAPIENS

<400> 2

Leu Val Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser  
1 5 10 15

Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln  
20 25 30

Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly  
35 40 45

<210> 3

<211> 33

<212> DNA

<213> HOMO SAPIENS

<400> 3  
gatgtcttct gggccctcct gtggaacaca gtt

33

<210> 4  
<211> 11  
<212> PRT  
<213> HOMO SAPIENS

<400> 4

Asp Val Phe Trp Ala Leu Leu Trp Asn Thr Val  
1 5 10

<210> 5  
<211> 746  
<212> DNA  
<213> HOMO SAPIENS

<400> 5  
gtggcccgagg agggcgccgag gccaggtagg tgcgatgggc gtgcagcccc ccaacttctc 60  
ctgggtgctt cggggccggc tggcgggact ggcgctgccg cggctccccg cccactacca 120  
gttcctgttg gaactgggag tgcggcacct ggtgtccctg acggagcgcg ggccccctca 180  
cagcgacagc tgccccggcc tcacctgca ccgcctgcgc atccccgact tctgcccggc 240  
ggcccccgac cagatcgacc gcttcgtgca gatcgtggac gaggccaacg cacggggaga 300  
ggctgtggga gtgcactgtg ctctgggctt tggcgcact ggcacatgc tggcctgtta 360  
cctggtgaag gagcggggct tggctgcagg agatgccatt gctgaaatcc gacgactacg 420  
accggccccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480  
gaaataaggg gccttagtac cttctacca ggccctcact ccccttcccc atgttgtcga 540  
tggggccaga gatgaaggga agtggactaa agtattaaac cctctagctc ccattggctg 600  
aagacactga agtagccac ccctgcaggc aggtcctgat tgaaggggag gcttgtactg 660  
ctttgttgaa taaatgagtt ttacgaacca gggaaaaaaaa aaaaaaaaaa aaagaaaaaa 720  
aaaaaaaaaa aaaaaaaaaa aaagaa 746

<210> 6  
<211> 248  
<212> PRT  
<213> HOMO SAPIENS

<220>  
<221> VARIANT  
<222> (160)..(160)  
<223> wherein 'Xaa' is any amino acid.

<220>  
<221> VARIANT  
<222> (200)..(200)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (202)..(202)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (214)..(214)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> VARIANT

<222> (223)..(223)

<223> wherein 'Xaa' is any amino acid.

<400> 6

Trp Pro Gly Arg Arg Arg Gly Gln Val Gly Ala Met Gly Val Gln Pro  
1 5 10 15

Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu Ala Gly Leu Ala Leu  
20 25 30

Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg  
35 40 45

His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys  
50 55 60

Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro  
65 70 75 80

Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn  
85 90 95

Ala Arg Gly Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg  
100 105 110

Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala  
115 120 125

Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Pro Ile  
130 135 140

Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr  
145 150 155 160

Lys Xaa Gly Ala Leu Val Pro Phe Tyr Gln Ala Leu Thr Pro Leu Pro  
165 170 175

His Val Val Asp Gly Ala Arg Asp Glu Gly Lys Trp Thr Lys Val Leu  
180 185 190

Asn Pro Leu Ala Pro Ile Gly Xaa Arg His Xaa Ser Ser Pro Pro Leu  
195 200 205

Gln Ala Gly Pro Asp Xaa Arg Gly Gly Leu Tyr Cys Phe Val Glu Xaa  
 210 215 220

Met Ser Phe Thr Asn Gln Gly Lys Lys Lys Lys Lys Lys Arg Lys Lys  
 225 230 235 240

Lys Lys Lys Lys Lys Lys Lys Arg  
 245

<210> 7  
 <211> 511  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 7  
 atggctagaa tgaacctccc tgcttctgtg gacattgcat acaaaaatgt gagatttctt 60  
 attacacaca acccaaccaa tacctacttt aatagattct tacaggaact taagcaggat 120  
 ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180  
 ggaagcatcc aggttccgga ctggcctttt gatgatggta cagcaccatc cagccagata 240  
 attgataact ggttaaaaact tatgaaaaat aaatttcatg aagatcctgg ttgttgtatt 300  
 gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgccc tagctttaat 360  
 tgaaggtgga atgaaatatg aaaatgtagt acagttcatc agataaaaagt gacatggaac 420  
 ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gcttgcacct 480  
 cagaaatccc agaaataact gtttccttca g 511

<210> 8  
 <211> 170  
 <212> PRT  
 <213> HOMO SAPIENS

<220>  
 <221> Variant  
 <222> (49)..(49)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (110)..(110)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (121)..(121)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (127)..(127)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (154)..(154)

<223> wherein 'Xaa' is any amino acid.

<400> 8

Met Ala Arg Met Asn Leu Pro Ala Ser Val Asp Ile Ala Tyr Lys Asn  
1 5 10 15

Val Arg Phe Leu Ile Thr His Asn Pro Thr Asn Thr Tyr Phe Asn Arg  
20 25 30

Phe Leu Gln Glu Leu Lys Gln Asp Gly Val Thr Thr Ile Val Arg Val  
35 40 45

Xaa Lys Ala Thr Tyr Asn Ile Ala Leu Leu Glu Lys Gly Ser Ile Gln  
50 55 60

Val Pro Asp Trp Pro Phe Asp Asp Gly Thr Ala Pro Ser Ser Gln Ile  
65 70 75 80

Ile Asp Asn Trp Leu Lys Leu Met Lys Asn Lys Phe His Glu Asp Pro  
85 90 95

Gly Cys Cys Ile Ala Ile His Cys Val Val Gly Phe Gly Xaa Ala Pro  
100 105 110

Val Ala Ser Cys Pro Ser Phe Asn Xaa Arg Trp Asn Glu Ile Xaa Lys  
115 120 125

Cys Ser Thr Val His Gln Ile Lys Val Thr Trp Asn Phe Xaa Gln Gln  
130 135 140

Thr Thr Phe Val Phe Gly Glu Ile Leu Ser Xaa Asn Met Leu Ala Pro  
145 150 155 160

Gln Lys Ser Gln Lys Xaa Leu Phe Pro Ser  
165 170

<210> 9

<211> 1710

<212> DNA

<213> HOMO SAPIENS

<400> 9

ctcaggcaga actatgaggc caagagtgcct catgcgcacc aggctttctt tttgaaattc 60

gaggagctga aggaggtgag caaggagcag ccagactgg aggctgagta ccctgccaac 120

accaccaaga actgttaacc acatgtgcta ccctatgacc actccagggt caggctgacc 180

cagctggagg gagagcctca ttctgactac atcaatgcc acttggtccc aggctacacc 240

cgccacagg agttcattgc ctctcagggg cctctcaaga aaacactgga gaacttctgg 300

cggctggtgc gggagcagca ggtccgcata atcatcatgc cgaccatcag catggagaac 360

```

gggaggggtgc tgtgtgagca ttactggctg accgactcta ccccgacac ccatgggtcac 420
atcaccatcc acctcctagc tgaggagcct gaggatgagt ggaccaagcg ggaattccag 480
ctgcagcacg ttgtccagca acatcaacgg aggggtggagc aactgcagtt caccacctga 540
tccgaccaca gcatccttga ggctcccagc tccctgctcg cctttatgga gctggtacag 600
tagcaggcaa gggccaccca gggcgtggga cccatcctgg tgcactgcag gggctgtccc 660
tgcgggtgtgg gcatgggccg gacaggcacc ttcgtggccc tgtcgaggct gctgcagcag 720
ctggaggagg agcagatggt agacgtgttc catgctgtgt atgcactccg gatgcaccag 780
cccctcatga tccagaccct gagccagtac gtcttcctgc acagctgcct actgaacaag 840
attctggaag gacccttcaa catctctgag tcttggccca tctctgtgac ggacctcccg 900
caggcgtgtg ccaagagggc agccagtgcc aatgctggct tcttgaagga gtacgaggcc 960
atcaaggacg aggtctggctt ttccgcacc cgcctggct atgagcagga cagccccgtc 1020
tcctatgacc gttctcaggg gcagttttct ccggtggagg agagcccccc tgacgacatg 1080
cctctctgga agccaatgat ctgtgctctg cagggtgggc cctctggcog tgatcatacg 1140
gtgctgactg gccccgcagg gccaaaggag ctctgggagc tgggtgtggca gcacagggtc 1200
catgtgcttg tctctctttg cccaccaat gtcattgaga aggaattctg gccaacggag 1260
atgcagcccg tagtcacaga catggtgacg gtgcactggg tggtgagag cagcacagca 1320
ggctggttct gtaccctcct cagggtcaca catggggaga gcaggaagga aaggagggtg 1380
cagagactgc aatttccata cctggagcct gggcatgagc tgcccgccac caccctgctg 1440
cccttcctgg ctgctgtggg ccagtgtctg tctcggggca acaacaagaa gccgggcaca 1500
ctgctcagcc actccaacaa ggggtgaacc cagctgggca ccttcctggc catggagcag 1560
ctgctgcagc aggcagggtc tgagtgcacc gtggatatct ttaacgtggc cctgcagcag 1620
tctcaggcct gtggccttat gacccaaca ctgaagcagt atgtctacct ctacaactgt 1680
ctgaacagcg cgctggcaga cgggctgccc 1710

```

<210> 10  
 <211> 570  
 <212> PRT  
 <213> HOMO SAPIENS

<220>  
 <221> Variant  
 <222> (46)..(46)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant

<222> (180)..(180)  
<223> wherein 'Xaa' is any amino acid.

<220>  
<221> Variant  
<222> (201)..(201)  
<223> wherein 'Xaa' is any amino acid.

<400> 10

Leu Arg Gln Asn Tyr Glu Ala Lys Ser Ala His Ala His Gln Ala Phe  
1 5 10 15  
Phe Leu Lys Phe Glu Glu Leu Lys Glu Val Ser Lys Glu Gln Pro Arg  
20 25 30  
Leu Glu Ala Glu Tyr Pro Ala Asn Thr Thr Lys Asn Cys Xaa Pro His  
35 40 45  
Val Leu Pro Tyr Asp His Ser Arg Val Arg Leu Thr Gln Leu Glu Gly  
50 55 60  
Glu Pro His Ser Asp Tyr Ile Asn Ala Asn Leu Val Pro Gly Tyr Thr  
65 70 75 80  
Arg Pro Gln Glu Phe Ile Ala Ser Gln Gly Pro Leu Lys Lys Thr Leu  
85 90 95  
Glu Asn Phe Trp Arg Leu Val Arg Glu Gln Gln Val Arg Ile Ile Ile  
100 105 110  
Met Pro Thr Ile Ser Met Glu Asn Gly Arg Val Leu Cys Glu His Tyr  
115 120 125  
Trp Leu Thr Asp Ser Thr Pro Asp Thr His Gly His Ile Thr Ile His  
130 135 140  
Leu Leu Ala Glu Glu Pro Glu Asp Glu Trp Thr Lys Arg Glu Phe Gln  
145 150 155 160  
Leu Gln His Val Val Gln Gln His Gln Arg Arg Val Glu Gln Leu Gln  
165 170 175  
Phe Thr Thr Xaa Ser Asp His Ser Ile Leu Glu Ala Pro Ser Ser Leu  
180 185 190  
Leu Ala Phe Met Glu Leu Val Gln Xaa Gln Ala Arg Ala Thr Gln Gly  
195 200 205  
Val Gly Pro Ile Leu Val His Cys Arg Gly Cys Pro Cys Gly Val Gly  
210 215 220  
Met Gly Arg Thr Gly Thr Phe Val Ala Leu Ser Arg Leu Leu Gln Gln  
225 230 235 240  
Leu Glu Glu Glu Gln Met Val Asp Val Phe His Ala Val Tyr Ala Leu  
245 250 255  
Arg Met His Gln Pro Leu Met Ile Gln Thr Leu Ser Gln Tyr Val Phe





<212> DNA  
<213> HOMO SAPIENS

<400> 11  
ctcaggcaga actatgagggc caagagtgct catgcgacc aggctttctt tttgaaattc 60  
gag 63

<210> 12  
<211> 91  
<212> DNA  
<213> HOMO SAPIENS

<400> 12  
gagctgaagg aggtgagcaa ggagcagccc agactggagg ctgagtaccc tgccaacacc 60  
accaagaact gttaaccaca tgtgctaccc t 91

<210> 13  
<211> 77  
<212> DNA  
<213> HOMO SAPIENS

<400> 13  
atgaccactc cagggtcagg ctgaccacgc tggagggaga gcctcattct gactacatca 60  
atgccaaactt ggtccca 77

<210> 14  
<211> 135  
<212> DNA  
<213> HOMO SAPIENS

<400> 14  
ggctacaccc gccacagga gttcattgcc tctcaggggc ctctcaagaa aacctggag 60  
aacttctggc ggctggtgcg ggagcagcag gtccgcatca tcatcatgcc gaccatcagc 120  
atggagaacg ggagg 135

<210> 15  
<211> 123  
<212> DNA  
<213> HOMO SAPIENS

<400> 15  
gtgctgtgtg agcattactg gctgaccgac tctaccccg acaccoatgg tcacatcacc 60  
atccacctcc tagctgagga gcctgaggat gagtggacca agcgggaatt ccagctgcag 120  
cac 123

<210> 16  
<211> 161  
<212> DNA  
<213> HOMO SAPIENS

<400> 16  
gttggtccagc aacatcaacg gaggggtggag caactgcagt tcaccacctg atccgaccac 60  
agcatccttg agggtcccag ctccctgctc gcctttatgg agctggtaca gtagcaggca 120  
agggccaccc agggcggtggg acccatcctg gtgcactgca g 161

<210> 17  
<211> 151  
<212> DNA  
<213> HOMO SAPIENS

<400> 17  
gggctgtccc tgcggtgtgg gcatgggccc gacaggcacc ttctgtggccc tgtcgaggct 60  
gctgcagcag ctggaggagg agcagatggt agacgtgttc catgctgtgt atgcactccg 120  
gatgcaccag cccctcatga tccagaccct g 151

<210> 18  
<211> 68  
<212> DNA  
<213> HOMO SAPIENS

<400> 18  
agccagtacg tcttcctgca cagctgccta ctgaacaaga ttctggaagg acccttcaac 60  
atctctga 68

<210> 19  
<211> 88  
<212> DNA  
<213> HOMO SAPIENS

<400> 19  
gtcttggccc atctctgtga cggacctccc gcaggcgtgt gccaagaggg cagccagtgc 60  
caatgctggc ttcttgaagg agtacgag 88

<210> 20  
<211> 67  
<212> DNA  
<213> HOMO SAPIENS

<400> 20  
gccatcaagg acgaggctgg cttttccgca ccccccgcctg gctatgagca ggacagcccc 60  
gtctcct 67

<210> 21  
<211> 58  
<212> DNA  
<213> HOMO SAPIENS

<400> 21

atgaccgttc tcaggggcag ttttctccgg tggaggagag cccccctgac gacatgcc 58

<210> 22  
 <211> 160  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 22  
 tctctggaag ccaatgatct gtgctctgca gggtagggccc tctggccgtg atcatacggg 60  
 gctgactggc cccgcagggc caaaggagct ctgggagctg gtgtggcagc acagggctca 120  
 tgtgcttgct tctcttttgc cacccaatgt catggagaag 160

<210> 23  
 <211> 111  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 23  
 gaattctggc caacggagat gcagcccgta gtcacagaca tggtagcggg gactgggtg 60  
 gctgagagca gcacagcagg ctggttctgt accctcctca gggtcacaca t 111

<210> 24  
 <211> 164  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 24  
 ggggagagca ggaaggaaag ggaggtgcag agactgcaat ttccatacct ggagcctggg 60  
 catgagctgc ccgccaccac cctgctgccc ttcttggtg ctgtgggcca gtgctgctct 120  
 cggggcaaca acaagaagcc gggcacactg ctcagccact ccaa 164

<210> 25  
 <211> 136  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 25  
 caaggggtgca acccagctgg gcaccttcct ggccatggag cagctgctgc agcaggcagg 60  
 gtctgagtgc accgtggata tctttaacgt ggccctgcag cagtctcagg cctgtggcct 120  
 tatgacccca aactg 136

<210> 26  
 <211> 57  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 26  
 aagcagtatg tctacctcta caactgtctg aacagcgcgc tggcagacgg gctgccc 57

<210> 27  
 <211> 1188  
 <212> PRT  
 <213> HOMO SAPIENS

<400> 27

Met	Gly	His	Leu	Pro	Thr	Gly	Ile	His	Gly	Ala	Arg	Arg	Leu	Leu	Pro	1	5	10	15
Leu	Leu	Trp	Leu	Phe	Val	Leu	Phe	Lys	Asn	Ala	Thr	Ala	Phe	His	Val	20	25	30	
Thr	Val	Gln	Asp	Asp	Asn	Asn	Ile	Val	Val	Ser	Leu	Glu	Ala	Ser	Asp	35	40	45	
Val	Ile	Ser	Pro	Ala	Ser	Val	Tyr	Val	Val	Lys	Ile	Thr	Gly	Glu	Ser	50	55	60	
Lys	Asn	Tyr	Phe	Phe	Glu	Phe	Glu	Glu	Phe	Asn	Ser	Thr	Leu	Pro	Pro	65	70	75	80
Pro	Val	Ile	Phe	Lys	Ala	Ser	Tyr	His	Gly	Leu	Tyr	Tyr	Ile	Ile	Thr	85	90	95	
Leu	Val	Val	Val	Asn	Gly	Asn	Val	Val	Thr	Lys	Pro	Ser	Arg	Ser	Ile	100	105	110	
Thr	Val	Leu	Thr	Lys	Pro	Leu	Pro	Val	Thr	Ser	Val	Ser	Ile	Tyr	Asp	115	120	125	
Tyr	Lys	Pro	Ser	Pro	Glu	Thr	Gly	Val	Leu	Phe	Glu	Ile	His	Tyr	Pro	130	135	140	
Glu	Lys	Tyr	Asn	Val	Phe	Thr	Arg	Val	Asn	Ile	Ser	Tyr	Trp	Glu	Gly	145	150	155	160
Lys	Asp	Phe	Arg	Thr	Met	Leu	Tyr	Lys	Asp	Phe	Phe	Lys	Gly	Lys	Thr	165	170	175	
Val	Phe	Asn	His	Trp	Leu	Pro	Gly	Met	Cys	Tyr	Ser	Asn	Ile	Thr	Phe	180	185	190	
Gln	Leu	Val	Ser	Glu	Ala	Thr	Phe	Asn	Lys	Ser	Thr	Leu	Val	Glu	Tyr	195	200	205	
Ser	Gly	Val	Ser	His	Glu	Pro	Lys	Gln	His	Arg	Thr	Ala	Pro	Tyr	Pro	210	215	220	
Pro	Gln	Asn	Ile	Ser	Val	Arg	Ile	Val	Asn	Leu	Asn	Lys	Asn	Asn	Trp	225	230	235	240
Glu	Glu	Gln	Ser	Gly	Asn	Phe	Pro	Glu	Glu	Ser	Phe	Met	Arg	Ser	Gln	245	250	255	
Asp	Thr	Ile	Gly	Lys	Glu	Lys	Leu	Phe	His	Phe	Thr	Glu	Glu	Thr	Pro	260	265	270	
Glu	Ile	Pro	Ser	Gly	Asn	Ile	Ser	Ser	Gly	Trp	Pro	Asp	Phe	Asn	Ser	275	280	285	





930

935

940

Pro Tyr Asp Phe Ser Arg Val Arg Leu Val Ser Met Asn Glu Glu Glu  
 945 950 955 960

Gly Ala Asp Tyr Ile Asn Ala Asn Tyr Ile Pro Gly Tyr Asn Ser Pro  
 965 970 975

Gln Glu Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu Thr Arg Asn Asp  
 980 985 990

Phe Trp Lys Met Val Leu Gln Gln Lys Ser Gln Ile Ile Val Met Leu  
 995 1000 1005

Thr Gln Cys Asn Glu Lys Arg Arg Val Lys Cys Asp His Tyr Trp  
 1010 1015 1020

Pro Phe Thr Glu Glu Pro Ile Ala Tyr Gly Asp Ile Thr Val Glu  
 1025 1030 1035

Met Ile Ser Glu Glu Glu Gln Asp Asp Trp Ala Cys Arg His Phe  
 1040 1045 1050

Arg Ile Asn Tyr Ala Asp Glu Met Gln Asp Val Met His Phe Asn  
 1055 1060 1065

Tyr Thr Ala Trp Pro Asp His Gly Val Pro Thr Ala Asn Ala Ala  
 1070 1075 1080

Glu Ser Ile Leu Gln Phe Val His Met Val Arg Gln Gln Ala Thr  
 1085 1090 1095

Lys Ser Lys Gly Pro Met Ile Ile His Cys Ser Ala Gly Val Gly  
 1100 1105 1110

Arg Thr Gly Thr Phe Ile Ala Leu Asp Arg Leu Leu Gln His Ile  
 1115 1120 1125

Arg Asp His Glu Phe Val Asp Ile Leu Gly Leu Val Ser Glu Met  
 1130 1135 1140

Arg Ser Tyr Arg Met Ser Met Val Gln Thr Glu Glu Gln Tyr Ile  
 1145 1150 1155

Phe Ile His Gln Cys Val Gln Leu Met Trp Met Lys Lys Lys Gln  
 1160 1165 1170

Gln Phe Cys Ile Ser Asp Val Ile Tyr Glu Asn Val Ser Lys Ser  
 1175 1180 1185

&lt;210&gt; 28

&lt;211&gt; 405

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 28

Met Val Thr Glu Val Asn Pro Asn Val Val Val Ile Ser Val Leu Ala  
 1 5 10 15

Ile Leu Ser Thr Leu Leu Ile Gly Leu Leu Leu Val Thr Leu Val Ile







Val His Cys Ser Ala Gly Cys Gly Arg Thr Gly Thr Phe Met Ala Leu  
 225 230 235 240

Phe Glu Ile Leu Ser Gln Thr Asp Asp Ser Thr Ser Thr Ser Lys Phe  
 245 250 255

Glu Val Asp Asn Ile Ala Asn Ile Val Ser Ser Leu Arg Ser Gln Arg  
 260 265 270

Met Gln Ser Val Gln Ser Val Asp Gln Leu Val Phe Leu Tyr Thr Val  
 275 280 285

Ser Gln Glu Leu Leu Gln Gly Lys Glu Phe Leu Leu Pro Gln Leu  
 290 295 300

<210> 30  
 <211> 580  
 <212> PRT  
 <213> homo sapiens

<400> 30

Met Lys Asp Arg Leu Tyr Phe Ala Thr Leu Arg Asn Arg Pro Lys Ser  
 1 5 10 15

Thr Val Asn Thr His Tyr Phe Ser Ile Asp Glu Glu Leu Val Tyr Glu  
 20 25 30

Asn Phe Tyr Ala Asp Phe Gly Pro Leu Asn Leu Ala Met Val Tyr Arg  
 35 40 45

Tyr Cys Cys Lys Leu Asn Lys Lys Leu Lys Ser Tyr Ser Leu Ser Arg  
 50 55 60

Lys Lys Ile Val His Tyr Thr Cys Phe Asp Gln Arg Lys Arg Ala Asn  
 65 70 75 80

Ala Ala Phe Leu Ile Gly Ala Tyr Ala Val Ile Tyr Leu Lys Lys Thr  
 85 90 95

Pro Glu Glu Ala Tyr Arg Ala Leu Leu Ser Gly Ser Asn Pro Pro Tyr  
 100 105 110

Leu Pro Phe Arg Asp Ala Ser Phe Gly Asn Cys Thr Tyr Asn Leu Thr  
 115 120 125

Ile Leu Asp Cys Leu Gln Gly Ile Arg Lys Gly Leu Gln His Gly Phe  
 130 135 140

Phe Asp Phe Glu Thr Ile Asp Val Asp Glu Tyr Glu His Tyr Glu Arg  
 145 150 155 160

Val Glu Asn Gly Asp Phe Asn Cys Ile Val Pro Gly Lys Phe Leu Ala  
 165 170 175

Phe Ser Gly Pro His Pro Lys Ser Lys Ile Glu Asn Gly Tyr Pro Leu  
 180 185 190

His Ala Pro Glu Ala Tyr Phe Pro Tyr Phe Lys Lys His Asn Val Thr  
 195 200 205





Ile Ala Phe Cys Gly Pro His Ser Arg Ala Arg Leu Glu Ser Gly Tyr  
 225 230 235 240  
 His Gln His Ser Pro Glu Thr Tyr Ile Gln Tyr Phe Lys Asn His Asn  
 245 250 255  
 Val Thr Thr Ile Ile Arg Leu Asn Lys Arg Met Tyr Asp Ala Lys Arg  
 260 265 270  
 Phe Thr Asp Ala Gly Phe Asp His His Asp Leu Phe Phe Ala Asp Gly  
 275 280 285  
 Ser Thr Pro Thr Asp Ala Ile Val Lys Glu Phe Leu Asp Ile Cys Glu  
 290 295 300  
 Asn Ala Glu Gly Ala Ile Ala Val His Cys Lys Ala Gly Leu Gly Arg  
 305 310 315 320  
 Thr Gly Thr Leu Ile Ala Cys Tyr Ile Met Lys His Tyr Arg Met Thr  
 325 330 335  
 Ala Ala Glu Thr Ile Ala Trp Val Arg Ile Cys Arg Pro Gly Ser Val  
 340 345 350  
 Ile Gly Pro Gln Gln Gln Phe Leu Val Met Lys Gln Thr Asn Leu Trp  
 355 360 365  
 Leu Glu Gly Asp Tyr Phe Arg Gln Lys Leu Lys Gly Gln Glu Asn Gly  
 370 375 380  
 Gln His Arg Ala Ala Phe Ser Lys Leu Leu Ser Gly Val Asp Asp Ile  
 385 390 395 400  
 Ser Ile Asn Gly Val Glu Asn Gln Asp Gln Gln Glu Pro Glu Pro Tyr  
 405 410 415  
 Ser Asp Asp Asp Glu Ile Asn Gly Val Thr Gln Gly Asp Arg Leu Arg  
 420 425 430  
 Ala Leu Lys Ser Arg Arg Gln Ser Lys Thr Asn Ala Ile Pro Leu Thr  
 435 440 445  
 Leu Ser Ile Ser Arg Thr Lys Thr Val Leu Arg  
 450 455

<210> 32  
 <211> 551  
 <212> PRT  
 <213> *Saccharomyces cerevisiae*

<400> 32

Met Arg Arg Ser Val Tyr Leu Asp Asn Thr Ile Glu Phe Leu Arg Gly  
 1 5 10 15  
 Arg Val Tyr Leu Gly Ala Tyr Asp Tyr Thr Pro Glu Asp Thr Asp Glu  
 20 25 30  
 Leu Val Phe Phe Thr Val Glu Asp Ala Ile Phe Tyr Asn Ser Phe His  
 35 40 45

Leu 50	Asp	Phe	Gly	Pro	Met	Asn 55	Ile	Gly	His	Leu 60	Tyr	Arg	Phe	Ala	Val
Ile 65	Phe	His	Glu	Ile	Leu 70	Asn	Asp	Pro	Glu	Asn 75	Ala	Asn	Lys	Ala	Val 80
Val	Phe	Tyr	Ser	Ser 85	Ala	Ser	Thr	Arg	Gln 90	Arg	Ala	Asn	Ala	Ala 95	Cys
Met	Leu	Cys	Cys 100	Tyr	Met	Ile	Leu	Val 105	Gln	Ala	Trp	Thr	Pro 110	His	Gln
Val	Leu	Gln 115	Pro	Leu	Ala	Gln	Val 120	Asp	Pro	Pro	Phe	Met 125	Pro	Phe	Arg
Asp	Ala 130	Gly	Tyr	Ser	Asn	Ala 135	Asp	Phe	Glu	Ile	Thr 140	Ile	Gln	Asp	Val
Val 145	Tyr	Gly	Val	Trp	Arg 150	Ala	Lys	Glu	Lys	Gly 155	Leu	Ile	Asp	Leu	His 160
Ser	Phe	Asn	Leu	Glu 165	Ser	Tyr	Glu	Lys	Tyr 170	Glu	His	Val	Glu	Phe 175	Gly
Asp	Phe	Asn	Val 180	Leu	Thr	Pro	Asp	Phe 185	Ile	Ala	Phe	Ala	Ser 190	Pro	Gln
Glu	Asp	His 195	Pro	Lys	Gly	Tyr	Leu 200	Ala	Thr	Lys	Ser	Ser 205	His	Leu	Asn
Gln	Pro 210	Phe	Lys	Ser	Val	Leu 215	Asn	Phe	Phe	Ala	Asn 220	Asn	Asn	Val	Gln
Leu 225	Val	Val	Arg	Leu	Asn 230	Ser	His	Leu	Tyr	Asn 235	Lys	Lys	His	Phe	Glu 240
Asp	Ile	Gly	Ile	Gln 245	His	Leu	Asp	Leu	Ile 250	Phe	Glu	Asp	Gly	Thr 255	Cys
Pro	Asp	Leu	Ser 260	Ile	Val	Lys	Asn	Phe 265	Val	Gly	Ala	Ala	Glu 270	Thr	Ile
Ile	Lys	Arg 275	Gly	Gly	Lys	Ile	Ala 280	Val	His	Cys	Lys	Ala 285	Gly	Leu	Gly
Arg	Thr 290	Gly	Cys	Leu	Ile	Gly 295	Ala	His	Leu	Ile	Tyr 300	Thr	Tyr	Gly	Phe
Thr 305	Ala	Asn	Glu	Cys	Ile 310	Gly	Phe	Leu	Arg	Phe 315	Ile	Arg	Pro	Gly	Met 320
Val	Val	Gly	Pro	Gln 325	Gln	His	Trp	Leu	Tyr 330	Leu	His	Gln	Asn	Asp 335	Phe
Arg	Glu	Trp	Lys 340	Tyr	Thr	Thr	Arg	Ile 345	Ser	Leu	Lys	Pro	Ser 350	Glu	Ala
Ile	Gly	Gly 355	Leu	Tyr	Pro	Leu	Ile 360	Ser	Leu	Glu	Glu	Tyr 365	Arg	Leu	Gln
Lys	Lys	Lys	Leu	Lys	Asp	Asp	Lys	Arg	Val	Ala	Gln	Asn	Asn	Ile	Glu



Val Leu Val Ala Leu Ala Leu Ile Glu Gly Gly Met Lys Tyr Glu Asp  
 115 120 125

Ala Val Gln Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys  
 130 135 140

Gln Leu Leu Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe  
 145 150 155 160

Lys Asp Ser Asn Gly His Arg Asn Asn Cys Cys Ile Gln  
 165 170

<210> 34  
 <211> 167  
 <212> PRT  
 <213> homo sapiens

<400> 34

Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe  
 1 5 10 15

Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu  
 20 25 30

Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala  
 35 40 45

Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp  
 50 55 60

Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp  
 65 70 75 80

Trp Leu Asn Leu Leu Lys Thr Lys Phe Arg Glu Glu Pro Gly Cys Cys  
 85 90 95

Val Ala Val His Cys Val Ala Gly Leu Gly Arg Ala Pro Val Leu Val  
 100 105 110

Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln  
 115 120 125

Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu  
 130 135 140

Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr  
 145 150 155 160

Asn Gly His Cys Cys Val Gln  
 165

<210> 35  
 <211> 167  
 <212> PRT  
 <213> Mus musculus

<400> 35



Met Asn Arg Pro Ala Pro Val Glu Ile Ser Tyr Glu Asn Met Arg Phe  
 1 5 10 15  
 Leu Ile Thr His Asn Pro Thr Asn Ala Thr Leu Asn Lys Phe Thr Glu  
 20 25 30  
 Glu Leu Lys Lys Tyr Gly Val Thr Thr Leu Val Arg Val Cys Asp Ala  
 35 40 45  
 Thr Tyr Asp Lys Ala Pro Val Glu Lys Glu Gly Ile His Val Leu Asp  
 50 55 60  
 Trp Pro Phe Asp Asp Gly Ala Pro Pro Pro Asn Gln Ile Val Asp Asp  
 65 70 75 80  
 Trp Leu Asn Leu Leu Lys Thr Leu Phe Arg Glu Glu Pro Gly Cys Cys  
 85 90 95  
 Val Ala Val His Cys Val Ala Gly Ile Gly Arg Ala Pro Val Leu Val  
 100 105 110  
 Ala Leu Ala Leu Ile Glu Cys Gly Met Lys Tyr Glu Asp Ala Val Gln  
 115 120 125  
 Phe Ile Arg Gln Lys Arg Arg Gly Ala Phe Asn Ser Lys Gln Leu Leu  
 130 135 140  
 Tyr Leu Glu Lys Tyr Arg Pro Lys Met Arg Leu Arg Phe Arg Asp Thr  
 145 150 155 160  
 Asn Gly His Cys Cys Val Gln  
 165

<210> 36  
 <211> 178  
 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 36

Met Ser Ile Thr Met Arg Gln Lys Asp Leu Arg Pro Ala Pro Ala Leu  
 1 5 10 15  
 Ile Glu Tyr Lys Gly Met Lys Phe Leu Ile Thr Asp Arg Pro Ser Asp  
 20 25 30  
 Ile Thr Ile Asn His Tyr Ile Met Glu Leu Lys Lys Asn Asn Val Asn  
 35 40 45  
 Thr Val Val Arg Val Cys Glu Pro Ser Tyr Asn Thr Asp Glu Leu Glu  
 50 55 60  
 Thr Gln Gly Ile Thr Val Lys Asp Leu Ala Phe Glu Asp Gly Thr Phe  
 65 70 75 80  
 Pro Pro Gln Gln Val Val Asp Glu Trp Phe Glu Phe Phe Val Val Leu  
 85 90 95  
 Tyr Arg Tyr Gln Gln Asn Pro Glu Ala Cys Val Ala Val His Cys Val  
 100 105 110



Lys	Thr	Ser	Ile	Leu	Gln	Trp	Thr	Glu	Pro	Val	Pro	Pro	Asp	His	Leu
210						215					220				
Thr	Leu	Arg	Ala	Leu	Gly	Thr	Ser	Ser	Leu	Gln	Ala	Phe	Trp	Asn	Ser
225					230					235					240
Ser	Glu	Gly	Ala	Thr	Trp	Phe	His	Leu	Ile	Leu	Thr	Asp	Leu	Leu	Glu
				245					250					255	
Gly	Thr	Asn	Leu	Thr	Lys	Val	Val	Arg	Gln	Gly	Ile	Ser	Thr	His	Thr
			260					265					270		
Phe	Leu	Arg	Leu	Ser	Pro	Gly	Thr	Pro	Tyr	Gln	Leu	Lys	Ile	Cys	Ala
		275					280					285			
Ala	Ala	Gly	Pro	His	Gln	Ile	Trp	Gly	Pro	Asn	Ala	Thr	Glu	Trp	Thr
290						295					300				
Tyr	Pro	Ser	Tyr	Pro	Ser	Asp	Leu	Val	Leu	Thr	Pro	Leu	Trp	Asn	Glu
305					310					315					320
Leu	Trp	Ala	Ser	Trp	Lys	Ala	Gly	Gln	Gly	Ala	Arg	Asp	Gly	Tyr	Val
				325					330					335	
Leu	Lys	Leu	Ser	Gly	Pro	Val	Glu	Asn	Thr	Thr	Thr	Leu	Gly	Pro	Glu
			340					345					350		
Glu	Cys	Asn	Ala	Val	Phe	Pro	Gly	Pro	Leu	Pro	Pro	Gly	His	Tyr	Thr
		355					360					365			
Leu	Gly	Leu	Arg	Val	Leu	Ala	Gly	Pro	Tyr	Asp	Ala	Trp	Val	Glu	Gly
	370					375					380				
Ser	Ile	Trp	Leu	Ala	Glu	Ser	Ala	Ala	Arg	Pro	Met	Glu	Val	Pro	Gly
385					390					395					400
Ala	Arg	Leu	Trp	Leu	Glu	Gly	Leu	Glu	Ala	Thr	Lys	Gln	Pro	Gly	Arg
				405					410					415	
Arg	Ala	Leu	Leu	Tyr	Ser	Val	Asp	Ala	Pro	Gly	Leu	Leu	Gly	Asn	Ile
			420					425					430		
Ser	Val	Ser	Ser	Gly	Ala	Thr	His	Val	Thr	Phe	Cys	Gly	Leu	Val	Pro
		435					440					445			
Gly	Ala	His	Tyr	Arg	Val	Asp	Ile	Ala	Ser	Ser	Met	Gly	Asp	Ile	Thr
	450					455					460				
Gln	Ser	Leu	Thr	Gly	Tyr	Thr	Ser	Pro	Leu	Pro	Pro	Gln	Ser	Leu	Glu
465					470					475					480
Ile	Ile	Ser	Arg	Asn	Ser	Pro	Ser	Asp	Leu	Thr	Ile	Gly	Trp	Ala	Pro
				485					490					495	
Ala	Pro	Gly	Gln	Met	Glu	Gly	Tyr	Lys	Val	Thr	Trp	His	Gln	Asp	Gly
			500					505					510		
Ser	Gln	Arg	Ser	Pro	Gly	Asp	Leu	Val	Asp	Leu	Gly	Pro	Asp	Ile	Ser
		515					520					525			
Ser	Leu	Thr	Leu	Lys	Ser	Leu	Val	Pro	Gly	Ser	Cys	Tyr	Thr	Val	Ser







Pro	Ala	Asp	Asn	Met	Leu	Ala	Ala	Ser	Leu	Phe	Pro	Gly	Gly	Pro
1490						1495					1500			
Ser	Gly	Arg	Asp	His	Val	Val	Leu	Thr	Gly	Ser	Ala	Gly	Pro	Lys
1505						1510					1515			
Glu	Leu	Trp	Glu	Met	Val	Trp	Glu	His	Gly	Ala	Tyr	Val	Leu	Val
1520						1525					1530			
Ser	Leu	Gly	Leu	Pro	Asp	Thr	Lys	Glu	Lys	Pro	Gln	Asp	Ile	Trp
1535						1540					1545			
Pro	Met	Glu	Met	Gln	Pro	Ile	Val	Thr	Asp	Met	Val	Thr	Val	His
1550						1555					1560			
Arg	Val	Ala	Glu	Ser	Asn	Thr	Ala	Gly	Trp	Pro	Ser	Thr	Leu	Ile
1565						1570					1575			
Arg	Val	Ile	His	Gly	Asp	Ser	Gly	Thr	Glu	Arg	Gln	Val	Gln	Cys
1580						1585					1590			
Leu	Gln	Phe	Pro	His	Cys	Glu	Thr	Gly	Ser	Glu	Leu	Pro	Ala	Asn
1595						1600					1605			
Thr	Leu	Leu	Thr	Phe	Leu	Asp	Ala	Val	Gly	Gln	Cys	Cys	Ser	Arg
1610						1615					1620			
Gly	Asn	Ser	Lys	Lys	Pro	Gly	Thr	Leu	Leu	Ser	His	Ser	Ser	Lys
1625						1630					1635			
Val	Thr	Asn	Gln	Leu	Ser	Thr	Phe	Leu	Ala	Met	Glu	Gln	Leu	Leu
1640						1645					1650			
Gln	Gln	Ala	Gly	Thr	Glu	Arg	Thr	Val	Asp	Val	Phe	Ser	Val	Ala
1655						1660					1665			
Leu	Lys	Gln	Thr	Gln	Ala	Cys	Gly	Leu	Lys	Thr	Pro	Thr	Leu	Glu
1670						1675					1680			
Gln	Tyr	Ile	Tyr	Leu	Tyr	Asn	Cys	Leu	Asn	Ser	Ala	Leu	Arg	Asn
1685						1690					1695			
Arg	Leu	Pro	Arg	Ala	Arg	Lys								
1700						1705								

<210> 38  
 <211> 1711  
 <212> PRT  
 <213> Rattus norvegicus

<400> 38

Met	Arg	Pro	Leu	Ile	Leu	Leu	Ala	Ala	Leu	Leu	Trp	Leu	Gln	Gly	Phe
1				5					10					15	
Leu	Ala	Glu	Asp	Asp	Ala	Cys	Ser	Ser	Leu	Gly	Gly	Ser	Pro	Asp	Arg
		20						25					30		
Gln	Gly	Gly	Gly	Pro	Leu	Leu	Ser	Val	Asn	Val	Ser	Ser	His	Gly	Lys









1010		1015		1020
Asp Cys 1025	Asp Asn Thr Gln	Glu 1030	Ile Cys Asn Gly	Arg Leu Lys Ser 1035
Gly Phe 1040	Gln Tyr Arg Phe	Ser 1045	Val Val Ala Phe	Ser Arg Leu Asn 1050
Thr Pro 1055	Glu Thr Ile Leu	Ala 1060	Phe Ser Ala Phe	Ser Glu Pro Arg 1065
Ala Ser 1070	Ile Ser Leu Ala	Ile 1075	Ile Pro Leu Thr	Val Met Leu Gly 1080
Ala Val 1085	Val Gly Ser Ile	Val 1090	Ile Val Cys Ala	Val Leu Cys Leu 1095
Leu Arg 1100	Trp Arg Cys Leu	Lys 1105	Gly Pro Arg Ser	Glu Lys Asp Gly 1110
Phe Ser 1115	Lys Glu Leu Met	Pro 1120	Tyr Asn Leu Trp	Arg Thr His Arg 1125
Pro Ile 1130	Pro Ile His Ser	Phe 1135	Arg Gln Ser Tyr	Glu Ala Lys Ser 1140
Ala His 1145	Ala His Gln Thr	Phe 1150	Phe Gln Glu Phe	Glu Glu Leu Lys 1155
Glu Val 1160	Gly Lys Asp Gln	Pro 1165	Arg Leu Glu Ala	Glu His Pro Asp 1170
Asn Ile 1175	Ile Lys Asn Arg	Tyr 1180	Pro His Val Leu	Pro Tyr Asp His 1185
Ser Arg 1190	Val Arg Leu Thr	Gln 1195	Leu Pro Gly Glu	Pro His Ser Asp 1200
Tyr Ile 1205	Asn Ala Asn Phe	Ile 1210	Pro Gly Tyr Ser	His Thr Gln Glu 1215
Ile Ile 1220	Ala Thr Gln Gly	Pro 1225	Leu Lys Lys Thr	Leu Glu Asp Phe 1230
Trp Arg 1235	Leu Val Trp Glu	Gln 1240	Gln Val His Val	Ile Ile Met Leu 1245
Thr Val 1250	Gly Met Glu Asn	Gly 1255	Arg Val Leu Cys	Glu His Tyr Trp 1260
Pro Ala 1265	Asn Ser Thr Pro	Val 1270	Thr His Gly His	Ile Thr Ile His 1275
Leu Leu 1280	Ala Glu Glu Pro	Glu 1285	Asp Glu Trp Thr	Arg Arg Glu Phe 1290
Gln Leu 1295	Gln His Gly Thr	Glu 1300	Gln Lys Gln Arg	Arg Val Lys Gln 1305
Leu Gln 1310	Phe Thr Thr Trp	Pro 1315	Asp His Ser Val	Pro Glu Ala Pro 1320







515				520				525							
Glu	Gly	Ala	Gln	Gly	Ala	Gly	Gly	Val	Leu	Phe	Ala	Pro	Phe	Gly	Arg
	530					535					540				
Ala	Gly	Ala	Pro	Gly	Pro	Gly	Gly	Gly	Ser	Asp	Leu	Arg	Arg	Arg	Glu
545					550					555					560
Ala	Ala	Arg	Ala	Glu	Pro	Arg	Asp	Ala	Arg	Thr	Gly	Trp	Pro	Glu	Glu
				565					570					575	
Pro	Ala	Pro	Glu	Thr	Gln	Phe	Lys	Arg	Arg	Ser	Cys	Gln	Met	Glu	Phe
			580					585					590		
Glu	Glu	Gly	Met	Val	Glu	Gly	Arg	Ala	Arg	Gly	Glu	Glu	Leu	Ala	Ala
		595					600					605			
Leu	Gly	Lys	Gln	Ala	Ser	Phe	Ser	Gly	Ser	Val	Glu	Val	Ile	Glu	Val
	610					615					620				
Ser															
625															
<210>	40														
<211>	663														
<212>	PRT														
<213>	Mus musculus														
<400>	40														
Met	Ala	Gly	Asp	Arg	Leu	Pro	Arg	Lys	Val	Met	Asp	Ala	Lys	Lys	Leu
1				5					10					15	
Ala	Ser	Leu	Leu	Arg	Gly	Gly	Pro	Gly	Gly	Pro	Leu	Val	Ile	Asp	Ser
			20					25					30		
Arg	Ser	Phe	Val	Glu	Tyr	Asn	Ser	Cys	His	Val	Leu	Ser	Ser	Val	Asn
		35					40					45			
Ile	Cys	Cys	Ser	Lys	Leu	Val	Lys	Arg	Arg	Leu	Gln	Gly	Lys	Val	
	50					55					60				
Thr	Ile	Ala	Glu	Leu	Ile	Gln	Pro	Ala	Thr	Arg	Ser	Gln	Val	Asp	Ala
65					70					75					80
Thr	Glu	Pro	Gln	Asp	Val	Val	Val	Tyr	Asp	Gln	Ser	Thr	Arg	Asp	Ala
				85					90					95	
Ser	Val	Leu	Ala	Ala	Asp	Ser	Phe	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Leu
			100					105					110		
Asp	Gly	Cys	Phe	Asp	Ser	Val	Ala	Ile	Leu	Thr	Gly	Gly	Phe	Ala	Thr
		115					120					125			
Phe	Ser	Ser	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Pro	Ala	Thr	Leu
	130					135					140				
Pro	Ser	Met	Ser	Leu	Ser	Gln	Pro	Cys	Leu	Pro	Val	Pro	Ser	Val	Gly
145					150					155					160
Leu	Thr	Arg	Ile	Leu	Pro	His	Leu	Tyr	Leu	Gly	Ser	Gln	Lys	Asp	Val

Leu	Asn	Lys	Asp	Leu	Met	Thr	Gln	Asn	Gly	Ile	Ser	Tyr	Val	Leu	Asn
			180					185					190		
Ala	Ser	Asn	Ser	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Cys	Glu	Ser	Arg	Phe
		195					200					205			
Met	Arg	Ile	Pro	Ile	Asn	Asp	Asn	Tyr	Cys	Glu	Lys	Leu	Leu	Pro	Trp
	210					215					220				
Leu	Asp	Lys	Ser	Ile	Glu	Phe	Ile	Asp	Lys	Ala	Lys	Leu	Ser	Ser	Cys
225					230					235					240
Gln	Val	Ile	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile
				245					250					255	
Ala	Ile	Ala	Tyr	Ile	Met	Lys	Thr	Met	Gly	Met	Ser	Ser	Asp	Asp	Ala
			260					265					270		
Tyr	Arg	Phe	Val	Lys	Asp	Arg	Arg	Pro	Ser	Ile	Ser	Pro	Asn	Phe	Asn
		275					280					285			
Phe	Leu	Gly	Gln	Leu	Leu	Glu	Tyr	Glu	Arg	Ser	Leu	Lys	Leu	Leu	Ala
	290					295					300				
Ala	Leu	Gln	Thr	Asp	Gly	Pro	His	Leu	Gly	Thr	Pro	Glu	Pro	Leu	Met
305					310					315					320
Gly	Pro	Ala	Ala	Gly	Ile	Pro	Leu	Pro	Arg	Leu	Pro	Pro	Ser	Thr	Ser
				325					330					335	
Glu	Ser	Ala	Ala	Thr	Gly	Ser	Glu	Ala	Ala	Thr	Ala	Ala	Arg	Glu	Gly
			340					345					350		
Ser	Pro	Ser	Ala	Gly	Gly	Asp	Ala	Pro	Ile	Pro	Ser	Thr	Ala	Pro	Ala
		355					360					365			
Thr	Ser	Ala	Leu	Gln	Gln	Gly	Leu	Arg	Gly	Leu	His	Leu	Ser	Ser	Asp
	370					375					380				
Arg	Leu	Gln	Asp	Thr	Asn	Arg	Leu	Lys	Arg	Ser	Phe	Ser	Leu	Asp	Ile
385					390					395					400
Lys	Ser	Ala	Tyr	Ala	Pro	Ser	Arg	Arg	Pro	Asp	Phe	Pro	Gly	Pro	Pro
			405						410				415		
Asp	Pro	Gly	Glu	Ala	Pro	Lys	Leu	Cys	Lys	Leu	Asp	Ser	Pro	Ser	Gly
			420					425					430		
Gly	Thr	Leu	Gly	Leu	Pro	Ser	Pro	Ser	Pro	Asp	Ser	Pro	Asp	Ser	Val
		435					440					445			
Pro	Glu	Cys	Arg	Pro	Arg	Pro	Arg	Arg	Arg	Arg	Pro	Pro	Ala	Ser	Ser
	450					455					460				
Pro	Ala	Arg	Ser	Pro	Ala	His	Gly	Leu	Gly	Leu	Asn	Phe	Gly	Asp	Thr
465					470					475					480
Ala	Arg	Gln	Thr	Pro	Arg	His	Gly	Leu	Ser	Ala	Leu	Ser	Ala	Pro	Gly
				485					490					495	





aattacagag	ctcatccagc	attcagcgaa	acataagggt	gacattgatt	gcagtcagaa	720
ggttgtagtt	tacgatcaaa	gctcccaaga	tggtgcctct	ctctcttcag	actgttttct	780
cactgtactt	ctgggtaaac	tggagaagag	cttcaactct	gttcacctgc	ttgcagggtg	840
gtttgctgag	ttctctcggt	gtttccctgg	cctctgtgaa	ggaaaatcca	ctctagtccc	900
tacctgcatt	tctcagcctt	gcttacctgt	tgccaacatt	gggccaaccc	gaattcttcc	960
caatctttat	cttggctgcc	agcgagatgt	cctcaacaag	gagctgatgc	agcagaatgg	1020
gattggttat	gtgttaaagt	ccagcaatac	ctgtccaaag	cctgacttta	tccccgagtc	1080
tcatttctctg	cgtgtgcctg	tgaatgacag	cttttgtgag	aaaattttgc	cgtgggttga	1140
caaatcagta	gatttcattg	agaaagcaaa	agcctccaat	ggatgtgttc	tagtgcactg	1200
tttagctggg	atctcccgtc	ccgccaccat	cgctatcgcc	tacatcatga	agaggatgga	1260
catgtcttta	gatgaagctt	acagatttgt	gaaagaaaaa	agacctacta	tatctccaaa	1320
cttcaatttt	ctggggccaa	tcctggccta	tgagaagaag	attaagaacc	agactggagc	1380
atcagggcca	aagagcaaac	tcaagctgct	gcccctggag	aagccaaatg	aacctgtccc	1440
tgctgtctca	gaggggtggc	agaaaagcga	gacgcccctc	agtccaccct	gtgccgactc	1500
tgctacctca	gaggcagcag	gacaaaggcc	cgtgcatccc	gccagcgtgc	ccagcgtgcc	1560
cagcgtgcag	ccgtcgtgtg	tagaggacag	cccgttggtg	caggcgtctc	gtgggctgca	1620
cctgtccgca	gacaggctgg	aagacagcaa	taagctcaag	cgctccttct	ctctggatat	1680
caaatcagtt	tcatattcag	ccagcatggc	agcatcctta	catggcttct	cctcatcaga	1740
agatgctttg	gaatactaca	aaccttcac	tactctggat	gggaccaaca	agctatgcc	1800
gttctcccct	gttcaggaac	tatcggagca	gactcccgaa	accagtcctg	ataaggagga	1860
agccagcatc	cccaagaagc	tgagaccgc	caggccttca	gacagccaga	gcaagcgatt	1920
gcattcggtc	agaaccagca	gcagtggcac	cgcccagagg	tcccttttat	ctccactgca	1980
tcgaagtggg	agcgtggagg	acaattacca	caccagcttc	cttttcggcc	tttccaccag	2040
ccagcagcac	ctcacgaagt	ctgctggcct	gggccttaag	ggctggcact	cggatatctt	2100
ggccccccag	acctctaccc	cttccttgac	cagcagctgg	tattttgcca	cagagtcttc	2160
acacttctac	tctgcctcag	ccatctacgg	aggcagtgcc	agttactctg	cctacagctg	2220
cagccagctg	cccacttgcg	gagaccaagt	ctattctgtg	cgcaggcggc	agaagccaag	2280
tgacagagct	gactcgcggc	ggagctggca	tgaagagagc	ccctttgaaa	agcagtttaa	2340
acgcagaagc	tgccaaatgg	aatttgagga	gagcatcatg	tcagagaaca	ggtcacggga	2400
agagctgggg	aaagtgggca	gtcagtcctag	cttttcgggc	agcatggaaa	tcattgaggt	2460

ctcctgagaa gaaagacact tgtgacttct atagacaatt tttttttctt gttcacaaaa	2520
aaattccctg ggaatctgaa atatgtatgt gggcatacat atatattttt ggaaaatgga	2580
gctatgggtgt aaaagcaaca ggtggatcaa cccagttggt actctcttaa catctgcatt	2640
tcagagatca gctaatactt gctctcaaca aaaatggaag ggcagatgct agaatcccc	2700
ctagacggag gaaaaccatt ttattcagtg aattacacat cctcttggtc ttaaaaaagc	2760
aagtgtcttt ggtgttggag gacaaaatcc cctaccattt tcacgttgtg ctactaagag	2820
atctcaaata ttagtctttg tccggaccct tccatagtag accttagcgc tgagactgag	2880
ccagcttggg ggtcaggtag gtagaccctg ttagggacag agcctagtgg taaatccaag	2940
agaaatgata ctatccaaag ctgattcaca aaccacgct cacctgacag ccgagggaca	3000
cgagcatcac tctgctggac ggaccattag gggccttgcc aagggtctacc ttagagcaaa	3060
cccagtagct cagacaggaa agtcggggct ttgaccacta ccatactctg tagcccattt	3120
tctaggcatt gtgaataggt aggtagctag tcacactttt cagaccaatt caaactgtct	3180
atgcacaaaa ttcccgtggg cctagatgga gataattttt ttttcttctc agctttatga	3240
agagaaggga aactgtctag gattcagctg aaccaccagg aacctggcaa catcacgatt	3300
taagotaagg ttgggaggct aacgagtcta cctccctctt tgtaaataca agaattgttt	3360
aaaatgggat tgtcaatcct ttaaataaag atgaacttgg tttcaagcca aatgtgaatt	3420
tatttgggtt ggtagcagag cagcagcacc ttcaaattct cagccaaagc agatgttttt	3480
gccctttctg cttcactgca tggatacagt tggtaaaatg taataatatg gcagaatttt	3540
ataggaaaact tcctagggag gtaaattatg ggaagattaa gaaaggtaga aattgctgag	3600
gagaagcagg aaacctgttt ccttagtggc ttttatcccc tcggcatgag atggggctga	3660
tgtttctata attgcctcag actttcacat ttactagtag ggctgagaga ggcttttagtg	3720
aggaaagaat attcagaata aaacggttga gaaagctgag aagaccattg agttttgata	3780
agttgtgaat agagtgcata gccatggcca agctgttttt ggaaacgctg gccggcgtgt	3840
cttcagtgga aaaagcaaat caaatggag cgagagcaaa ggggcgtcct cagtcctcaa	3900
cctacaatca ctgtatggaa tcggtcctgg cagctgaaca taggaggtca ctggaacaag	3960
tgatagtga gattggcttt caaacatcct cctggcttga gttttatcag ctacaatgtg	4020
ggtcctcttt tgaagcctta attcacaaca gcagcttttt gggggtgggg ctgggcgggt	4080
gttgtcattg ttctttccct tcctgtaagt gtcgctagtt gctgcctcgt atctcaggtt	4140
tttctctgtt tttgagaaat ggacagtttt ttgaccagga tgtgaattca tgtttcctat	4200
ggtgacttct aaaaccagca cagaatgata tgactcaaca cagaccgact tggttatggg	4260
gatgatgagc cgcacagacc tcactagttg tgcacaaata atgtgctatg atggggtgta	4320

```

aagtgaaggc agaagagggc cagccgcatt gttatgatac tgggaaagtg ccggtcaacg 4380
atttgagtta gtttttagat atacattgaa atctttaatc agacattctc aagtttcaca 4440
cagtagtttt tgatgttatg tacacacaca ccaaagtgtg aacagttcac cacttccaga 4500
gtgtgggtcat gcccaaaaca tgtttaagaa aggaaagcag tagctccttg ctaacgatgt 4560
ttcaggaggt ttggggcact tggttttaat gagcttctgt catttagggc ttctcttggc 4620
catgggtccc ttcttcttgg aactgtgatg tagtcacatc ctacagcctt tagtgctggt 4680
tcactagtgt cagataatca gttcttggaa tcgagactgc cgtggcgaag ggggtggcctc 4740
ggaggcaggc tctggagctg cttggatgtc tttaggtggg gtggtggctg gctctcttca 4800
gcatgtaatt ggggaaaccc tcgcgtctac taggggtgat acagatgggtg attttaaaga 4860
gcaaaactag acttctatgt gagaagtgtc ggaaaatgat ttaggacgtg taaagttaga 4920
tggaaagact gtaaatgttt aatatgaata tagtgttctt ttgaagtaag gccagctggt 4980
gaacgggttaa actgtgcatt tctcattttg atgtgtcatg tatgttaatg tatgaaatga 5040
ttaaataaaa tcaaaactgg tacctgttta tccataaaaa aaaaaaaaaa aaaaaaaaaa 5100
aaaaaaaaaa g 5111

```

```

<210> 42
<211> 665
<212> PRT
<213> HOMO SAPIENS

```

```

<400> 42

```

```

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val
1           5           10           15
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg
20           25           30
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile
35           40           45
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu
50           55           60
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp
65           70           75           80
Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala
85           90           95
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu
100          105          110
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe
115          120          125

```

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
 130 135 140  
 Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
 145 150 155 160  
 Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
 165 170 175  
 Lys Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
 180 185 190  
 Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
 195 200 205  
 Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
 210 215 220  
 Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240  
 Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255  
 Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270  
 Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu  
 275 280 285  
 Gly Gln Leu Leu Ala Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala  
 290 295 300  
 Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu Pro Leu Glu Lys Pro Asn  
 305 310 315 320  
 Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro  
 325 330 335  
 Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln  
 340 345 350  
 Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro  
 355 360 365  
 Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His  
 370 375 380  
 Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
 385 390 395 400  
 Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser  
 405 410 415  
 Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro  
 420 425 430  
 Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val  
 435 440 445  
 Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu



<212> DNA  
<213> HOMO SAPIENS

<400> 45  
tgacaatgga tagctacttt tccttcctgt aaggcaaagtc tcatcacctt caccatatct 60  
aggatagtag taagagacgc 80

<210> 46  
<211> 20  
<212> DNA  
<213> HOMO SAPIENS

<400> 46  
ttcggatgga aggattatgg 20

<210> 47  
<211> 18  
<212> DNA  
<213> HOMO SAPIENS

<400> 47  
ctgttcgacc aagccctg 18

<210> 48  
<211> 80  
<212> DNA  
<213> HOMO SAPIENS

<400> 48  
tgacaatgga tagctacttt tccttcctgt aaggcaaagtc tcatcacctt caccatatct 60  
aggatagtag taagagacgc 80

<210> 49  
<211> 19  
<212> DNA  
<213> HOMO SAPIENS

<400> 49  
ccaacttctc ctgggtgct 19

<210> 50  
<211> 18  
<212> DNA  
<213> HOMO SAPIENS

<400> 50  
ctccgtcagg gacaccag 18

<210> 51  
<211> 79  
<212> DNA  
<213> HOMO SAPIENS





ttaagttcct gtaagaatct	80
<210> 58	
<211> 20	
<212> DNA	
<213> HOMO SAPIENS	
<400> 58	
tgcttctgtg gacattgcat	20
<210> 59	
<211> 20	
<212> DNA	
<213> HOMO SAPIENS	
<400> 59	
aacctggatg cttcccttct	20
<210> 60	
<211> 80	
<212> DNA	
<213> HOMO SAPIENS	
<400> 60	
aaaagagcaa tggttgtaagt tgcttttcat actcttacta tggtggtaac tccatcctgc	60
ttaagttcct gtaagaatct	80
<210> 61	
<211> 20	
<212> DNA	
<213> HOMO SAPIENS	
<400> 61	
ggcagaacta tgaggccaag	20
<210> 62	
<211> 20	
<212> DNA	
<213> HOMO SAPIENS	
<400> 62	
gaccctggag tggatcatagg	20
<210> 63	
<211> 80	
<212> DNA	
<213> HOMO SAPIENS	
<400> 63	
gctcatgcgc accaggcttt ctttttgaaa ttcgaggagc tgaaggaggt gagcaaggag	60
cagcccagac tggaggctga	80

<210> 64  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 64  
 gcaaccaggct ttctttttga 20

<210> 65  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 65  
 gaccctggag tggcatagg 20

<210> 66  
 <211> 80  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 66  
 tcgaggagct gaaggaggtg agcaaggagc agcccagact ggaggctgag taccctgcca 60  
 acaccaccaa gaactgttaa 80

<210> 67  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 67  
 atgggaccaa caagctatgc 20

<210> 68  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 68  
 ttatcaggac tggtttcggg 20

<210> 69  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

<400> 69  
 ggccaaagag caaactcaag 20

<210> 70  
 <211> 20  
 <212> DNA  
 <213> HOMO SAPIENS

CCDS:CCDS1000.1

```

<400> 70
gcatagcttg ttggtcccat 20

<210> 71
<211> 20
<212> DNA
<213> HOMO SAPIENS

<400> 71
aggcagaact atgaggccaa 20

<210> 72
<211> 20
<212> DNA
<213> HOMO SAPIENS

<400> 72
gaccctggag tggatcatagg 20

<210> 73
<211> 80
<212> DNA
<213> HOMO SAPIENS

<400> 73
gctcatgcgc accaggcttt ctttttgaaa ttcgaggagc tgaaggaggt gagcaaggag 60
cagcccagac tggaggctga 80

<210> 74
<211> 80
<212> DNA
<213> HOMO SAPIENS

<400> 74
tcagcctcca gtctgggctg ctccttgctc acctccttca gctcctcgaa tttcaaaaag 60
aaagcctggg gcgcatgagc 80

<210> 75
<211> 8
<212> PRT
<213> bacteriophage T7

<400> 75
Asp Tyr Lys Asp Asp Asp Lys
1 5

<210> 76
<211> 733
<212> DNA
<213> homo sapiens

<400> 76
gggatccgga gcccaaactc tctgacaaaa ctcacacatg cccaccgtgc ccagcacctg 60

```



<213> HOMO SAPIENS

<220>

<221> Variant

<222> (5)..(5)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (6)..(6)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (7)..(7)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (8)..(8)

<223> wherein 'Xaa' is any amino acid.

<400> 79

Ile Val Val Met Xaa Xaa Xaa Xaa Glu  
1 5

<210> 80

<211> 8

<212> PRT

<213> HOMO SAPIENS

<400> 80

Asp Asn Tyr Ile Asn Ala Ser Asn  
1 5

<210> 81

<211> 6

<212> PRT

<213> HOMO SAPIENS

<220>

<221> Variant

<222> (2)..(2)

<223> wherein 'Xaa' is any amino acid.

<220>

<221> Variant

<222> (3)..(3)

<223> wherein 'Xaa' is any amino acid.

<400> 81

Cys Xaa Xaa Tyr Trp Pro

1

5

<210> 82  
 <211> 9  
 <212> PRT  
 <213> HOMO SAPIENS

<220>  
 <221> Variant  
 <222> (5)..(5)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (6)..(6)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (7)..(7)  
 <223> wherein 'Xaa' is any amino acid.

<220>  
 <221> Variant  
 <222> (8)..(8)  
 <223> wherein 'Xaa' is any amino acid.

<400> 82

Ile Val Val Met Xaa Xaa Xaa Xaa Glu  
 1 5

<210> 83  
 <211> 511  
 <212> DNA  
 <213> homo sapiens

<400> 83  
 atggctagaa tgaacctccc tgcttctgtg gacattgcat acaaaaatgt gagatttctt 60  
 attacacaca acccaaccaa tacctacttt aatagattct tacaggaact taagcaggat 120  
 ggagttacca ccatagtaag agtatgaaaa gcaacttaca acattgctct tttagagaag 180  
 ggaagcatcc aggttccgga ctggcctttt gatgatggta cagcaccatc cagccagata 240  
 attgataact gggttaaaact tatgaaaaat aaatttcatg aagatcctgg ttgttgtatt 300  
 gcaattcact gtgttgtagg ttttgggtga gctccagttg ctagttgcc tagctttaat 360  
 tgaagggtgga atgaaatatg aaaatgtagt acagttcatc agataaaagt gacatggaac 420  
 ttttaacagc aaacaacttt tgtatttgga gaaatattgt cttaaaatat gottgcacct 480  
 cagaaatccc agaaataact gtttccttca g 511

<210> 84  
 <211> 167  
 <212> PRT  
 <213> homo sapiens

<400> 84

Met	Ala	Arg	Met	Asn	Leu	Pro	Ala	Ser	Val	Asp	Ile	Ala	Tyr	Lys	Asn
1				5					10					15	
Val	Arg	Phe	Leu	Ile	Thr	His	Asn	Pro	Thr	Asn	Thr	Tyr	Phe	Asn	Arg
			20					25					30		
Phe	Leu	Gln	Glu	Leu	Lys	Gln	Asp	Gly	Val	Thr	Thr	Ile	Val	Arg	Val
		35					40					45			
Lys	Ala	Thr	Tyr	Asn	Ile	Ala	Leu	Leu	Glu	Lys	Gly	Ser	Ile	Gln	Val
	50					55					60				
Pro	Asp	Trp	Pro	Phe	Asp	Asp	Gly	Thr	Ala	Pro	Ser	Ser	Gln	Ile	Ile
65					70					75					80
Asp	Asn	Trp	Leu	Lys	Leu	Met	Lys	Asn	Lys	Phe	His	Glu	Asp	Pro	Gly
				85					90					95	
Cys	Cys	Ile	Ala	Ile	His	Cys	Val	Val	Gly	Phe	Gly	Glu	Leu	Gln	Leu
			100					105					110		
Leu	Val	Ala	Leu	Ala	Leu	Ile	Glu	Gly	Gly	Met	Lys	Tyr	Glu	Asn	Val
		115					120					125			
Val	Gln	Phe	Ile	Arg	Lys	His	Gly	Thr	Phe	Asn	Ser	Lys	Gln	Leu	Leu
	130					135					140				
Tyr	Leu	Glu	Lys	Tyr	Cys	Leu	Lys	Ile	Cys	Leu	His	Leu	Arg	Asn	Pro
145					150					155					160
Arg	Asn	Asn	Cys	Phe	Leu	Gln									
				165											

<210> 85  
 <211> 14  
 <212> PRT  
 <213> homo sapiens

<400> 85

Pro	Phe	Val	Glu	Tyr	Asn	Thr	Ser	His	Ile	Leu	Glu	Ala	Ile
1				5					10				

<210> 86  
 <211> 14  
 <212> PRT  
 <213> homo sapiens

<400> 86

Glu	Ala	Ile	Asn	Ile	Asn	Cys	Ser	Lys	Leu	Met	Lys	Arg	Arg
1			5						10				

<210> 87

<211> 14  
<212> PRT  
<213> homo sapiens

<400> 87

Ile Gly Tyr Val Leu Asn Ala Ser Asn Thr Cys Pro Lys Pro  
1 5 10

<210> 88  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 88

Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu  
1 5 10

<210> 89  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 89

Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys  
1 5 10

<210> 90  
<211> 14  
<212> PRT  
<213> homo sapiens

<400> 90

Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys  
1 5 10

<210> 91  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 91

Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu  
1 5 10

<210> 92  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 92

Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp  
1 5 10

<210> 93  
<211> 13



<212> PRT  
<213> homo sapiens  
  
<400> 93

Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile  
1 5 10

<210> 94  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 94

Val Asp Ile Asp Cys Ser Gln Lys Val Val Val Tyr Asp  
1 5 10

<210> 95  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 95

Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
1 5 10

<210> 96  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 96

Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser  
1 5 10

<210> 97  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 97

Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln  
1 5 10

<210> 98  
<211> 13  
<212> PRT  
<213> homo sapiens

<400> 98

Pro Ser Asp Ser Gln Ser Lys Arg Leu His Ser Val Arg  
1 5 10

<210> 99  
<211> 13  
<212> PRT

<213> homo sapiens

<400> 99

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly  
1 5 10

<210> 100

<211> 13

<212> PRT

<213> homo sapiens

<400> 100

Gly Asp Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro  
1 5 10

<210> 101

<211> 13

<212> PRT

<213> homo sapiens

<400> 101

Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser Arg Arg  
1 5 10

<210> 102

<211> 13

<212> PRT

<213> homo sapiens

<400> 102

Ser Asp Arg Ala Asp Ser Arg Arg Ser Trp His Glu Glu  
1 5 10

<210> 103

<211> 23

<212> PRT

<213> homo sapiens

<400> 103

Asn Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala  
1 5 10 15

Thr Ile Ala Ile Ala Tyr Ile  
20

<210> 104

<211> 39

<212> DNA

<213> Homo sapiens

<400> 104

gcagcagcgg ccgcatcgcc tacatcatga agaggatgg

39

<210> 105

<211> 37

```

<212> DNA
<213> Homo sapiens

<400> 105
gcagcagtcg acggagacct caatgatttc catgctg 37

<210> 106
<211> 39
<212> DNA
<213> Homo sapiens

<400> 106
gcagcagcgg ccgcatggcc catgagatga ttggaactc 39

<210> 107
<211> 37
<212> DNA
<213> Homo sapiens

<400> 107
gcagcagtcg acctgcacgc tgggcacgct gggcacg 37

<210> 108
<211> 5450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (538)..(2532)

<400> 108
gaaaagaaga cgaggaggag agcgacggga cgggacgcga gcgggagcgc agccgccctc 60
tcggctccgc ggcggcgcct cgcaagtccg ggaggcgagg ggggcccagag gggagacgcc 120
gtgacaactt tcgtttccct ctgagggaat tgggaggtcg gcggcccaa aagctttcag 180
tccagtgtaa agctgttgga gcgcgggagc aaaggtaaag aatgatgtaa tgcgctggct 240
gtcccaaagc atcttttggt gtggaatggt tattccagtc atctctttat gaatcaaatg 300
tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga 360
gacattcact tggagggctc ttgctgaaaa tgggtttaac tctccttttg ccagtcacca 420
ccagcctgac ctcatacact tttagtacaa tggagtggct gagcctttga gcacaccacc 480
attacatcat cgtggcaaat taaagaagga ggtgggaaaa gaggacttat tgttgtc 537
atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg 585
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val
1 5 10 15
gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg 633
Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg
20 25 30

```

cca ttt gtg gaa tac aat aca tcc cac att ttg gaa gcc att aat atc	681
Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile	
35 40 45	
aac tgc tcc aag ctt atg aag cga agg ttg caa cag gac aaa gtg tta	729
Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu	
50 55 60	
att aca gag ctc atc cag cat tca gcg aaa cat aag gtt gac att gat	777
Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp	
65 70 75 80	
tgc agt cag aag gtt gta gtt tac gat caa agc tcc caa gat gtt gcc	825
Cys Ser Gln Lys Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala	
85 90 95	
tct ctc tct tca gac tgt ttt ctc act gta ctt ctg ggt aaa ctg gag	873
Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu	
100 105 110	
aag agc ttc aac tct gtt cac ctg ctt gca ggt ggg ttt gct gag ttc	921
Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe	
115 120 125	
tct cgt tgt ttc cct ggc ctc tgt gaa gga aaa tcc act cta gtc cct	969
Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro	
130 135 140	
acc tgc att tct cag cct tgc tta cct gtt gcc aac att ggg cca acc	1017
Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr	
145 150 155 160	
cga att ctt ccc aat ctt tat ctt ggc tgc cag cga gat gtc ctc aac	1065
Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn	
165 170 175	
aag gag ctg ata cag cag aat ggg att ggt tat gtg tta aat gcc agc	1113
Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser	
180 185 190	
tat acc tgt cca aag cct gac ttt atc ccc gag tct cat ttc ctg cgt	1161
Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg	
195 200 205	
gtg cct gtg aat gac agc ttt tgt gag aaa att ttg ccg tgg ttg gac	1209
Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp	
210 215 220	
aaa tca gta gat ttc att gag aaa gca aaa gcc tcc aat gga tgt gtt	1257
Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val	
225 230 235 240	
cta gtg cac tgt tta gct ggg atc tcc cgc tcc gcc acc atc gct atc	1305
Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile	
245 250 255	
gcc tac atc atg aag agg atg gac atg tct tta gat gaa gct tac aga	1353
Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg	
260 265 270	
ttt gtg aaa gaa aaa aga cct act ata tct cca aac ttc aat ttt ctg	1401





gatggagata	atTTTTTTTT	cttctcagct	ttatgaagag	aagggaaaact	gtctaggatt	3332
cagctgaacc	accaggaacc	tggcaacatc	acgatttaag	ctaagggttg	gaggctaacg	3392
agtctacctc	cctcttttga	aatcaaagaa	ttgttttaaaa	tgggattgtc	aatcctttta	3452
ataaagatga	acttggtttc	aagccaaatg	tgaattttatt	tgggttggtg	gcagagcagc	3512
agcaccttca	aattctcagc	caaagcagat	gtttttgccc	tttctgcttc	actgcatgga	3572
tacagttggt	aaaatgtaat	aatatggcag	aatttttatag	gaaacttcct	agggaggtaa	3632
attatgggaa	gattaagaaa	ggtacaaatt	gctgaggaga	agcaggaaac	ctgtttcctt	3692
agtggctttt	atccccctcg	catgcgatgg	ggctgatgtt	tctatgattg	cctcagactt	3752
tcacattttac	tagtagggct	gagagaggct	ttagttagga	aggaatattc	agaataaaac	3812
ggttgagaaa	gctgagaaga	ccattgagtt	ttgatcagtt	gtgaatagag	tgcaaagcca	3872
tggccaagct	gttttttgaa	acgctggccg	gcgtgtcttc	agtggaaaaa	gcaaatacaa	3932
atggagcgag	agcaaagggg	cgtcctcagt	cctcaaccta	caatcactgt	atggaatcgg	3992
tcctggcagc	tgaacatagg	aggtcactgg	aacaagtgat	agtgcagatt	ggctttcaaa	4052
catcctcctg	gcttgagttt	tatcagctac	aatgtgggtc	ctcttttgaa	gccttaattc	4112
acaacagcag	ctttttgggg	gtggggctgg	gcgggtgttg	tcattgttct	ttcccttcct	4172
gtaagtgtcg	ctagttgctg	cctcgtatct	caggtttttc	tctgtttttg	agaaatggac	4232
agttttttga	ccaggatgtg	acttcatgtt	tcctatggtg	acttctaaaa	ccagcacaga	4292
atgatatgac	tcaacacaga	ccgacttggt	tatggggatg	atgagccgca	cagacctcac	4352
tagttgtgca	caaataatgt	gctatgatgg	ggtgtaaagt	gaaggcagaa	gagggtcagc	4412
cgcattgtta	tgatactggg	aaagtgctgg	tcaacgattt	gagttagttt	ttagatatac	4472
attgaaatct	ttaatcagac	attctcaagt	ttcacacagt	agtttttgat	gttatgtaca	4532
cacacaccaa	atgtgtaaca	gttcaccact	tccagagtgt	ggatcatgcc	aaaacatggt	4592
taagaaagga	aagcagtagc	tccttgctaa	cgatgtttca	ggaggtttgg	ggcacttggt	4652
tttaatgagc	ttctgtcatt	tagggcttct	cttggccatg	gtcccccttc	ttctggaact	4712
gtgatgtagt	cacatcctac	agccttttagt	gctgggtcac	tagtgtcaga	taatcagttc	4772
ttggaatcga	gactgccgtg	gcgaaggggt	ggcctcggag	gcaggctctg	gagctgcttg	4832
gatgtcttta	ggtgggggtg	tggctggctc	tcttcagcat	gtaattgggg	aaaccctcgc	4892
gtctactagg	ggtgatacag	atggtgattt	taaagagcaa	aactagactt	ctatgtgaga	4952
agtgtctgaa	aatgatttag	gacatgtgta	aagtttagatg	gaaagactgt	aaatgtttta	5012
tatgaatata	gtgttccttt	gaagtaaggc	cagctgttga	acggttaaac	tgtgcatttc	5072

tcattttgat gtgtcatgta tgtaaatgta tgaaatgatt aaataaaaatc aaaactggta 5132  
cctgtttata cataaatacg agaaaagacc tatctttgca gccataaact cggtagggaac 5192  
accaccactc aagttgccaa aggaggcagt ggtgaaacct gtcctgttct cacttaaatg 5252  
aggatttagc tcaaaataaa gtggtggtgt catcaggttt attccgtgtt ctgtcattca 5312  
catggaacac cggatgatta gctaacagtt tagtgccagc cttcattctt tactgtgtac 5372  
gttaaatgca cactacagtg aaaaagccta agacacttgg taaatatttt ctagctgact 5432  
gattccagaa cacacaag 5450

<210> 109  
<211> 665  
<212> PRT  
<213> Homo sapiens

<400> 109

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
50 55 60

Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
65 70 75 80

Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
100 105 110

Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
145 150 155 160



Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
165 170 175

Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
180 185 190

Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
225 230 235 240

Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu  
275 280 285

Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala  
290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn  
305 310 315 320

Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro  
325 330 335

Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln  
340 345 350

Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro  
355 360 365

Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His  
370 375 380

Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe  
385 390 395 400

Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser  
405 410 415

Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro  
420 425 430

Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val  
435 440 445

Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu  
450 455 460

Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln  
465 470 475 480

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln  
485 490 495

Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn  
500 505 510

Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu  
515 520 525

Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu  
530 535 540

Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala  
545 550 555 560

Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser  
565 570 575

Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp  
580 585 590

Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp  
595 600 605

Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys  
610 615 620

Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn  
625 630 635 640

Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser

645

650

655

Gly Ser Met Glu Ile Ile Glu Val Ser  
660 665

<210> 110  
<211> 625  
<212> PRT  
<213> Homo sapiens

<400> 110

Met Ala Gly Asp Arg Leu Pro Arg Lys Val Met Asp Ala Lys Lys Leu  
1 5 10 15

Ala Ser Leu Leu Arg Gly Gly Pro Gly Gly Pro Leu Val Ile Asp Ser  
20 25 30

Arg Ser Phe Val Glu Tyr Asn Ser Trp His Val Leu Ser Ser Val Asn  
35 40 45

Ile Cys Cys Ser Lys Leu Val Lys Arg Arg Leu Gln Gln Gly Lys Val  
50 55 60

Thr Ile Ala Glu Leu Ile Gln Pro Ala Ala Arg Ser Gln Val Glu Ala  
65 70 75 80

Thr Glu Pro Gln Asp Val Val Val Tyr Asp Gln Ser Thr Arg Asp Ala  
85 90 95

Ser Val Leu Ala Ala Asp Ser Phe Leu Ser Ile Leu Leu Ser Lys Leu  
100 105 110

Asp Gly Cys Phe Asp Ser Val Ala Ile Leu Thr Gly Gly Phe Ala Thr  
115 120 125

Phe Ser Ser Cys Phe Pro Gly Leu Cys Glu Gly Lys Pro Ala Ala Leu  
130 135 140

Leu Pro Met Ser Leu Ser Gln Pro Cys Leu Pro Val Pro Ser Val Gly  
145 150 155 160

Leu Thr Arg Ile Leu Pro His Leu Tyr Leu Gly Ser Gln Lys Asp Val  
165 170 175

Leu Asn Lys Asp Leu Met Thr Gln Asn Gly Ile Ser Tyr Val Leu Asn  
180 185 190

Ala Ser Asn Ser Cys Pro Lys Pro Asp Phe Ile Cys Glu Ser Arg Phe  
195 200 205

Met Arg Val Pro Ile Asn Asp Asn Tyr Cys Glu Lys Leu Leu Pro Trp  
210 215 220

Leu Asp Lys Ser Ile Glu Phe Ile Asp Lys Ala Lys Leu Ser Ser Cys  
225 230 235 240

Gln Val Ile Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile  
245 250 255



Pro Ala Pro Glu Thr Gln Phe Lys Arg Arg Ser Cys Gln Met Glu Phe  
 580 585 590  
 Glu Glu Gly Met Val Glu Gly Arg Ala Arg Gly Glu Glu Leu Ala Ala  
 595 600 605  
 Leu Gly Lys Gln Ala Ser Phe Ser Gly Ser Val Glu Val Ile Glu Val  
 610 615 620  
 Ser  
 625  
 <210> 111  
 <211> 381  
 <212> PRT  
 <213> Homo sapiens  
 <400> 111  
 Met Ile Asp Thr Leu Arg Pro Val Pro Phe Ala Ser Glu Met Ala Ile  
 1 5 10 15  
 Ser Lys Thr Val Ala Trp Leu Asn Glu Gln Leu Glu Leu Gly Asn Glu  
 20 25 30  
 Arg Leu Leu Leu Met Asp Cys Arg Pro Gln Glu Leu Tyr Glu Ser Ser  
 35 40 45  
 His Ile Glu Ser Ala Ile Asn Val Ala Ile Pro Gly Ile Met Leu Arg  
 50 55 60  
 Arg Leu Gln Lys Gly Asn Leu Pro Val Arg Ala Leu Phe Thr Arg Gly  
 65 70 75 80  
 Glu Asp Arg Asp Arg Phe Thr Arg Arg Cys Gly Thr Asp Thr Val Val  
 85 90 95  
 Leu Tyr Asp Glu Ser Ser Ser Asp Trp Asn Glu Asn Thr Gly Gly Glu  
 100 105 110  
 Ser Leu Leu Gly Leu Leu Leu Lys Lys Leu Lys Asp Glu Gly Cys Arg  
 115 120 125  
 Ala Phe Tyr Leu Glu Gly Gly Phe Ser Lys Phe Gln Ala Glu Phe Ser  
 130 135 140  
 Leu His Cys Glu Thr Asn Leu Asp Gly Ser Cys Ser Ser Ser Ser Pro  
 145 150 155 160  
 Pro Leu Pro Val Leu Gly Leu Gly Gly Leu Arg Ile Ser Ser Asp Ser  
 165 170 175  
 Ser Ser Asp Ile Glu Ser Asp Leu Asp Arg Asp Pro Asn Ser Ala Thr  
 180 185 190  
 Asp Ser Asp Gly Ser Pro Leu Ser Asn Ser Gln Pro Ser Phe Pro Val  
 195 200 205  
 Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala Lys Asp Ser Thr Asn  
 210 215 220

Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr Ile Leu Asn Val Thr  
 225 230 235 240  
 Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly Glu Phe Lys Tyr Lys  
 245 250 255  
 Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn Leu Ser Gln Phe Phe  
 260 265 270  
 Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg Gly Lys Asn Cys Gly  
 275 280 285  
 Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Val Thr Val Thr  
 290 295 300  
 Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser Met Asn Asp Ala Tyr  
 305 310 315 320  
 Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser Pro Asn Phe Asn Phe  
 325 330 335  
 Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu Gly Leu Ser Ser Pro  
 340 345 350  
 Cys Asp Asn Arg Val Pro Ala Gln Gln Leu Tyr Phe Thr Thr Pro Ser  
 355 360 365  
 Asn Gln Asn Val Tyr Gln Val Asp Ser Leu Gln Ser Thr  
 370 375 380  
 <210> 112  
 <211> 482  
 <212> PRT  
 <213> Homo sapiens  
 <400> 112  
 Met Pro Pro Ser Pro Leu Asp Asp Arg Val Val Val Ala Leu Ser Arg  
 1 5 10 15  
 Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu  
 20 25 30  
 Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr  
 35 40 45  
 Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser  
 50 55 60  
 Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys  
 65 70 75 80  
 Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala  
 85 90 95  
 Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys  
 100 105 110  
 Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser  
 115 120 125

Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu  
 130 135 140  
 Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr  
 145 150 155 160  
 Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp  
 165 170 175  
 Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val  
 180 185 190  
 His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly  
 195 200 205  
 Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser  
 210 215 220  
 Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr  
 225 230 235 240  
 Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu  
 245 250 255  
 Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly  
 260 265 270  
 Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu  
 275 280 285  
 Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Ala Ala Ser  
 290 295 300  
 Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala  
 305 310 315 320  
 Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp  
 325 330 335  
 Ala Gln Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile  
 340 345 350  
 Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe  
 355 360 365  
 Asn Tyr Lys Arg Leu Pro Ala Thr Asp Ser Asn Lys Gln Asn Leu Arg  
 370 375 380  
 Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys  
 385 390 395 400  
 Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala  
 405 410 415  
 Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr  
 420 425 430  
 Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn  
 435 440 445  
 Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn

450

455

460

Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr  
 465 470 475 480

Val Val

<210> 113  
 <211> 2756  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (369)..(2348)

<400> 113  
 gactgaggtt gtcagcccag tgtaaagctg ttggagtggag ggcagaaagg taaaggatga 60  
 tgtaatgcct ggctgcccta gagcatcttt tgttggtggga tgggtattcc catcatctct 120  
 atgaatctag tgtgagggggc tgctttgtgg aaggaatcct ttgcaagagc atatcaacag 180  
 gaaagagaaa gagacattca gttggagggc tcttgctgaa atggatttaa ctctctcttt 240  
 gccagtcacc actagcctga cctcatacat ttttagtaca atggagtggc tgagcctttg 300  
 agcacagcac cattacatca tcgtggcaaa ttaaagaacg aggtgggggaa agaggactta 360  
 ttgttgtc atg gcc cat gag atg att gga act caa att gtt act gag agc 410  
 Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Ser  
 1 5 10  
 ttg gtg gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat 458  
 Leu Val Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp  
 15 20 25 30  
 agc cga cca ttt gtg gaa tac aat acg tct cac att ttg gaa gcc att 506  
 Ser Arg Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile  
 35 40 45  
 aat atc aac tgc tcc aaa ctg atg aag cga agg ttg caa cag gac aaa 554  
 Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys  
 50 55 60  
 gta tta att aca gaa cta atc cac caa tct aca aag cat aag gtt gac 602  
 Val Leu Ile Thr Glu Leu Ile His Gln Ser Thr Lys His Lys Val Asp  
 65 70 75  
 att gac tgc aat caa aga gtg gta gtt tat gat cac agt tca caa gat 650  
 Ile Asp Cys Asn Gln Arg Val Val Val Tyr Asp His Ser Ser Gln Asp  
 80 85 90  
 gtt ggt tct ctg tgc tca gac tgc ttt ctc act gta ctt ctg ggt aag 698  
 Val Gly Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys  
 95 100 105 110  
 ctg gag aga agc ttc aac tct gtc cac ctg ctt gca ggt ggc ttt gct 746  
 Leu Glu Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala  
 115 120 125



gag	ttc	tct	cgt	tgt	ttc	cct	ggc	ctc	tgt	gaa	gga	aag	tcc	act	cta	794
Glu	Phe	Ser	Arg	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Ser	Thr	Leu	
			130				135							140		
gtc	cct	acc	tgc	ata	tct	cag	cct	tgc	tta	cct	ggt	gcg	aac	att	ggg	842
Val	Pro	Thr	Cys	Ile	Ser	Gln	Pro	Cys	Leu	Pro	Val	Ala	Asn	Ile	Gly	
			145				150							155		
cca	act	cga	att	ctt	ccc	aat	ctc	tat	ctt	ggc	tgc	cag	cga	gat	gtc	890
Pro	Thr	Arg	Ile	Leu	Pro	Asn	Leu	Tyr	Leu	Gly	Cys	Gln	Arg	Asp	Val	
			160				165							170		
ctc	aac	aag	gac	ctg	atg	caa	cag	aat	ggg	att	ggc	tat	gtg	tta	aat	938
Leu	Asn	Lys	Asp	Leu	Met	Gln	Gln	Asn	Gly	Ile	Gly	Tyr	Val	Leu	Asn	
			175				180							185		
gcc	agc	aat	acc	tgt	cca	aag	cct	gac	ttc	ata	cct	gaa	tct	cac	ttc	986
Ala	Ser	Asn	Thr	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Pro	Glu	Ser	His	Phe	
			195				200							205		
ctg	cga	gtg	cct	gtg	aat	gac	agc	ttt	tgt	gag	aaa	atc	cta	cca	tgg	1034
Leu	Arg	Val	Pro	Val	Asn	Asp	Ser	Phe	Cys	Glu	Lys	Ile	Leu	Pro	Trp	
			210				215							220		
ttg	gac	aag	tct	gtg	gat	ttc	att	gag	aaa	gca	aaa	gcc	tcc	aat	ggc	1082
Leu	Asp	Lys	Ser	Val	Asp	Phe	Ile	Glu	Lys	Ala	Lys	Ala	Ser	Asn	Gly	
			225				230							235		
tgt	gtg	ctt	atc	cac	tgc	tta	gct	ggg	atc	tct	cgc	tcc	gcc	act	att	1130
Cys	Val	Leu	Ile	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	
			240				245							250		
gct	att	gcc	tac	atc	atg	aag	agg	atg	gac	atg	tct	cta	gat	gag	gct	1178
Ala	Ile	Ala	Tyr	Ile	Met	Lys	Arg	Met	Asp	Met	Ser	Leu	Asp	Glu	Ala	
			255				260							265		
tac	aga	ttt	gtg	aaa	gaa	aaa	aga	cct	act	ata	tct	ccg	aat	ttt	aat	1226
Tyr	Arg	Phe	Val	Lys	Glu	Lys	Arg	Pro	Thr	Ile	Ser	Pro	Asn	Phe	Asn	
			275				280							285		
ttt	atg	ggc	caa	ctc	atg	gac	tat	gag	aag	acg	att	aat	aac	cag	act	1274
Phe	Met	Gly	Gln	Leu	Met	Asp	Tyr	Glu	Lys	Thr	Ile	Asn	Asn	Gln	Thr	
			290				295							300		
gga	atg	tca	ggg	cca	aag	agc	aaa	ctg	aag	ctg	ctg	cac	cta	gac	aaa	1322
Gly	Met	Ser	Gly	Pro	Lys	Ser	Lys	Leu	Lys	Leu	Leu	His	Leu	Asp	Lys	
			305				310							315		
ccc	agt	gag	ccc	gtg	cct	gca	gcc	tca	gag	ggc	gga	tgg	aag	agt	gca	1370
Pro	Ser	Glu	Pro	Val	Pro	Ala	Ala	Ser	Glu	Gly	Gly	Trp	Lys	Ser	Ala	
			320				325							330		
ctg	tct	ctc	agt	cca	ccc	tgt	gcc	aac	tcg	acc	tcg	gag	gca	tca	ggg	1418
Leu	Ser	Leu	Ser	Pro	Pro	Cys	Ala	Asn	Ser	Thr	Ser	Glu	Ala	Ser	Gly	
			335				340							345		
caa	agg	ctt	gtg	cat	cct	gca	agt	gtg	ccc	cgc	tta	cag	ccg	tca	ctc	1466
Gln	Arg	Leu	Val	His	Pro	Ala	Ser	Val	Pro	Arg	Leu	Gln	Pro	Ser	Leu	
			355				360							365		



Ser Trp His	Glu Glu Ser	Pro Phe	Glu Lys Gln	Phe Lys	Arg Arg Ser	
	610		615		620	
tgc caa atg gaa ttt gga gag agc att atg tgc gag aac agg tcc agg						2282
Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg	625		630		635	
gag gag ctg ggc aag gtg ggc agc cag tcc agc ttc tcc ggc agc atg						2330
Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met	640		645		650	
gag atc atc gag gtc tct tgagaagacc tcgtcgcttc tgttgacagt						2378
Glu Ile Ile Glu Val Ser	655		660			
tttgttttcct gttcacaaaa aatagtcctt gtaaattctga aatatgtata tgtacatata						2438
tatatatattt tggaatatag agctacggta taaaagcaac agatggatca acacagttgt						2498
tctctcagca cctgcactga gaatagctaa ctctcagaaa agattggaag ggtagatggt						2558
agaattctcc cagccaggag aagagatttg gttcagtga ttgcacatct tcttgttcct						2618
acaaaagcaa gggttttggt tgtttgtatg ttgtttgttt ttaatgttag agggcaaaat						2678
ccctcccatt ttcacgtgca acagaggtct cagaactcat ctctgtccag gcccttcct						2738
agtgcacctt agcgctaa						2756

<210> 114  
 <211> 660  
 <212> PRT  
 <213> Mus musculus

<400> 114

Met Ala His	Glu Met Ile	Gly Thr Gln	Ile Val Thr	Glu Ser Leu	Val
1	5		10		15
Ala Leu Leu	Glu Ser Gly	Thr Glu Lys	Val Leu Leu	Ile Asp Ser	Arg
	20		25		30
Pro Phe Val	Glu Tyr Asn	Thr Ser His	Ile Leu Glu	Ala Ile Asn	Ile
	35		40		45
Asn Cys Ser	Lys Leu Met	Lys Arg Arg	Leu Gln Gln	Asp Lys Val	Leu
	50		55		60
Ile Thr Glu	Leu Ile His	Gln Ser Thr	Lys His Lys	Val Asp Ile	Asp
65		70		75	80
Cys Asn Gln	Arg Val Val	Val Tyr Asp	His Ser Ser	Gln Asp Val	Gly
	85		90		95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
 100 105 110

Arg Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
 115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
 130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
 145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
 165 170 175

Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
 180 185 190

Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
 195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
 210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240

Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Met  
 275 280 285

Gly Gln Leu Met Asp Tyr Glu Lys Thr Ile Asn Asn Gln Thr Gly Met  
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Asp Lys Pro Ser  
 305 310 315 320

Glu Pro Val Pro Ala Ala Ser Glu Gly Gly Trp Lys Ser Ala Leu Ser  
 325 330 335

Leu Ser Pro Pro Cys Ala Asn Ser Thr Ser Glu Ala Ser Gly Gln Arg

340

345

350

Leu Val His Pro Ala Ser Val Pro Arg Leu Gln Pro Ser Leu Leu Glu  
 355 360 365

Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu Gln Leu Ser Ser Glu  
 370 375 380

Lys Leu Glu Asp Ser Thr Lys Leu Lys Arg Ser Phe Ser Leu Asp Ile  
 385 390 395 400

Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu His Gly Phe  
 405 410 415

Ser Ser Glu Glu Ala Leu Asp Tyr Cys Lys Pro Ser Ala Thr Leu Asp  
 420 425 430

Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln Glu Val Ser Glu  
 435 440 445

Gln Ser Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala His Ile Pro Lys  
 450 455 460

Gln Pro Gln Pro Pro Arg Pro Ser Glu Ser Gln Val Thr Arg Leu His  
 465 470 475 480

Ser Val Arg Thr Gly Ser Ser Gly Ser Thr Gln Arg Pro Phe Phe Ser  
 485 490 495

Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr His Thr Asn Phe  
 500 505 510

Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr Lys Ser Ala Gly  
 515 520 525

Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala Pro Gln Ser Ser  
 530 535 540

Ala Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr Glu Pro Ser His  
 545 550 555 560

Leu Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Asn Ser Ser Tyr Ser Ala  
 565 570 575

Tyr Ser Cys Gly Gln Leu Pro Thr Cys Ser Asp Gln Ile Tyr Ser Val  
 580 585 590

Arg Arg Arg Gln Lys Pro Thr Asp Arg Ala Asp Ser Arg Arg Ser Trp  
 595 600 605

His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg Arg Ser Cys Gln  
 610 615 620

Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu  
 625 630 635 640

Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly Ser Met Glu Ile  
 645 650 655

Ile Glu Val Ser  
 660

<210> 115  
 <211> 408  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 acaatggagt ggctgagcct ttgagcacac caccattaca tcatcgtggc aaattaaaga 60  
 aggagggtggg aaaagaggac ttattgttgt catggcccat gagatgattg gaactcaaat 120  
 tgttactgag aggttggtgg ctctgctgga aagtggaacg gaaaaagtgc tgctaattga 180  
 tagccggcca tttgtggaat acaatacatc ccacattttg gaagccatta atatcaactg 240  
 ctccaagctt atgaagcgaa ggttgcaaca ggacaaagtg ttaattacag agctcatcca 300  
 gcattcagcg aaacataagg ttgacattga ttgcagtcag aaggttgtag tttagcatca 360  
 aagctcccaa gatgttgccct ctctctcttc agactgtttt ctcaactgt 408

<210> 116  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 116

Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala Leu Leu  
 1 5 10

<210> 117  
 <211> 13  
 <212> PRT  
 <213> Homo sapiens

<400> 117

Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp



<210> 124  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 124

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly  
1 5 10

<210> 125  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 125

Gly Asp Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro  
1 5 10

<210> 126  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 126

Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser Arg Arg  
1 5 10

<210> 127  
<211> 13  
<212> PRT  
<213> Homo sapiens

<400> 127

Ser Asp Arg Ala Asp Ser Arg Arg Ser Trp His Glu Glu  
1 5 10

<210> 128  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 128

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile  
1 5 10

<210> 129  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 129

Glu Ala Ile Asn Ile Asn Cys Ser Lys Leu Met Lys Arg Arg  
1 5 10



<210> 130  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 130

Ile Gly Tyr Val Leu Asn Ala Ser Tyr Thr Cys Pro Lys Pro  
1 5 10

<210> 131  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 131

Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu  
1 5 10

<210> 132  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 132

Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys  
1 5 10

<210> 133  
<211> 14  
<212> PRT  
<213> Homo sapiens

<400> 133

Ser Ile Met Ser Glu Asn Arg Ser Arg Glu Glu Leu Gly Lys  
1 5 10

<210> 134  
<211> 140  
<212> PRT  
<213> Homo sapiens

<400> 134

Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp  
1 5 10 15

Val Leu Asn Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu  
20 25 30

Asn Ala Ser Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His  
35 40 45

Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro  
50 55 60

Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn  
65 70 75 80

Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr  
85 90 95  
Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu  
100 105 110  
Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe  
115 120 125  
Asn Phe Leu Gly Gln Leu Leu Asp Tyr Glu Lys Lys  
130 135 140

<210> 135  
<211> 140  
<212> PRT  
<213> Mus musculus

<400> 135

Gly Pro Thr Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp  
1 5 10 15  
Val Leu Asn Lys Asp Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu  
20 25 30  
Asn Ala Ser Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His  
35 40 45  
Phe Leu Arg Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro  
50 55 60  
Trp Leu Asp Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn  
65 70 75 80  
Gly Cys Val Leu Ile His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr  
85 90 95  
Ile Ala Ile Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu  
100 105 110  
Ala Tyr Arg Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe  
115 120 125  
Asn Phe Met Gly Gln Leu Met Asp Tyr Glu Lys Thr  
130 135 140

<210> 136  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 136

gcagcagcgg ccgcattggg ccaacccgaa ttcttccc

38

<210> 137  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 137  
gcagcagtcg acggagacct caatgatttc catgctg 37

<210> 138  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 138  
gcagcagcgg ccgcatggcc catgagatga ttggaactc 39

<210> 139  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 139  
gcagcagtcg accttcttct catagtccag gagttgg 37

<210> 140  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 140  
gcagcagcgg ccgcattggg ccaactcgaa ttcttccc 38

<210> 141  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 141  
gcagcagtcg acagagacct cgatgatctc catgctg 37

<210> 142  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 142  
gcagcagcgg ccgcatggcc catgagatga ttggaactc 39

<210> 143  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 143  
gcagcagtcg accgtcttct catagtccat gagttgg 37

<210> 144  
<211> 23  
<212> PRT

<213> Homo sapiens

<400> 144

Asn Gly Cys Val Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala  
1 5 10 15

Thr Ile Ala Ile Ala Tyr Ile  
20

<210> 145  
<211> 25  
<212> DNA  
<213> Homo sapiens

<400> 145  
cacaccacca ttacatcatc gtggc 25

<210> 146  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 146  
tgctgctctg ctaccaaccc 20

<210> 147  
<211> 5450  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (538)..(2532)

<400> 147  
gaaaagaaga cgaggaggag agcgacggga cgggacgcga gcgggagcgc agccgccttc 60  
tcgggctccgc ggcgggcgctt cgcaagtccg ggaggcgagg gggggcccgag gggagacgcc 120  
gtgacaactt tcgtttccct ctgagggaaat tgggaggtcg gcggccccaa aagctttcag 180  
tccagtgtaa agctgttgga gcgcggggagc aaaggtaaag aatgatgtaa tgcgctggct 240  
gctccaaagc atcttttgtt gtggaatggt tattccagtc atctctttat gaatcaaattg 300  
tgaggggctg ctttgtggac ggagtccttt gcaagagcac atcaacggga aagagaaaga 360  
gacattcact tggagggtc ttgctgaaaa tgggtttaac tctccttttg ccagtcacca 420  
ccagcctgac ctcatcact ttagtagaaa tggagtggt gagcctttga gcacaccacc 480  
attacatcat cgtggcaaatt taaagaagga ggtgggaaaa gaggacttat tgttgtc 537  
atg gcc cat gag atg att gga act caa att gtt act gag agg ttg gtg 585  
Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

gct ctg ctg gaa agt gga acg gaa aaa gtg ctg cta att gat agc cgg 633

Ala	Leu	Leu	Glu	Ser	Gly	Thr	Glu	Lys	Val	Leu	Leu	Ile	Asp	Ser	Arg		
			20					25					30				
cca	ttt	gtg	gaa	tac	aat	aca	tcc	cac	att	ttg	gaa	gcc	att	aat	atc	681	
Pro	Phe	Val	Glu	Tyr	Asn	Thr	Ser	His	Ile	Leu	Glu	Ala	Ile	Asn	Ile		
		35					40				45						
aac	tgc	tcc	aag	ctt	atg	aag	cga	agg	ttg	caa	cag	gac	aaa	gtg	tta	729	
Asn	Cys	Ser	Lys	Leu	Met	Lys	Arg	Arg	Leu	Gln	Gln	Asp	Lys	Val	Leu		
	50					55					60						
att	aca	gag	ctc	atc	cag	cat	tca	gcg	aaa	cat	aag	gtt	gac	att	gat	777	
Ile	Thr	Glu	Leu	Ile	Gln	His	Ser	Ala	Lys	His	Lys	Val	Asp	Ile	Asp		
65					70				75						80		
tgc	agt	cag	aag	gtt	gta	gtt	tac	gat	caa	agc	tcc	caa	gat	gtt	gcc	825	
Cys	Ser	Gln	Lys	Val	Val	Val	Tyr	Asp	Gln	Ser	Ser	Gln	Asp	Val	Ala		
			85					90						95			
tct	ctc	tct	tca	gac	tgt	ttt	ctc	act	gta	ctt	ctg	ggt	aaa	ctg	gag	873	
Ser	Leu	Ser	Ser	Asp	Cys	Phe	Leu	Thr	Val	Leu	Leu	Gly	Lys	Leu	Glu		
			100					105					110				
aag	agc	ttc	aac	tct	gtt	cac	ctg	ctt	gca	ggt	ggg	ttt	gct	gag	ttc	921	
Lys	Ser	Phe	Asn	Ser	Val	His	Leu	Leu	Ala	Gly	Gly	Phe	Ala	Glu	Phe		
		115					120					125					
tct	cgt	tgt	ttc	cct	ggc	ctc	tgt	gaa	gga	aaa	tcc	act	cta	gtc	cct	969	
Ser	Arg	Cys	Phe	Pro	Gly	Leu	Cys	Glu	Gly	Lys	Ser	Thr	Leu	Val	Pro		
	130					135					140						
acc	tgc	att	tct	cag	cct	tgc	tta	cct	gtt	gcc	aac	att	ggg	cca	acc	1017	
Thr	Cys	Ile	Ser	Gln	Pro	Cys	Leu	Pro	Val	Ala	Asn	Ile	Gly	Pro	Thr		
145					150					155					160		
cga	att	ctt	ccc	aat	ctt	tat	ctt	ggc	tgc	cag	cga	gat	gtc	ctc	aac	1065	
Arg	Ile	Leu	Pro	Asn	Leu	Tyr	Leu	Gly	Cys	Gln	Arg	Asp	Val	Leu	Asn		
				165				170						175			
aag	gag	ctg	ata	cag	cag	aat	ggg	att	ggt	tat	gtg	tta	aat	gcc	agc	1113	
Lys	Glu	Leu	Ile	Gln	Gln	Asn	Gly	Ile	Gly	Tyr	Val	Leu	Asn	Ala	Ser		
			180				185						190				
tat	acc	tgt	cca	aag	cct	gac	ttt	atc	ccc	gag	tct	cat	ttc	ctg	cgt	1161	
Tyr	Thr	Cys	Pro	Lys	Pro	Asp	Phe	Ile	Pro	Glu	Ser	His	Phe	Leu	Arg		
		195				200						205					
gtg	cct	gtg	aat	gac	agc	ttt	tgt	gag	aaa	att	ttg	ccg	tgg	ttg	gac	1209	
Val	Pro	Val	Asn	Asp	Ser	Phe	Cys	Glu	Lys	Ile	Leu	Pro	Trp	Leu	Asp		
	210					215					220						
aaa	tca	gta	gat	ttc	att	gag	aaa	gca	aaa	gcc	tcc	aat	gga	tgt	gtt	1257	
Lys	Ser	Val	Asp	Phe	Ile	Glu	Lys	Ala	Lys	Ala	Ser	Asn	Gly	Cys	Val		
225					230					235					240		
cta	gtg	cac	tgt	tta	gct	ggg	atc	tcc	cgc	tcc	gcc	acc	atc	gct	atc	1305	
Leu	Val	His	Cys	Leu	Ala	Gly	Ile	Ser	Arg	Ser	Ala	Thr	Ile	Ala	Ile		
				245				250						255			
gcc	tac	atc	atg	aag	agg	atg	gac	atg	tct	tta	gat	gaa	gct	tac	aga	1353	
Ala	Tyr	Ile	Met	Lys	Arg	Met	Asp	Met	Ser	Leu	Asp	Glu	Ala	Tyr	Arg		

260						265						270						
ttt	gtg	aaa	gaa	aaa	aga	cct	act	ata	tct	cca	aac	ttc	aat	ttt	ctg	1401		
Phe	Val	Lys	Glu	Lys	Arg	Pro	Thr	Ile	Ser	Pro	Asn	Phe	Asn	Phe	Leu			
		275				280				285								
ggc	caa	ctc	ctg	gac	tat	gag	aag	aag	att	aag	aac	cag	act	gga	gca	1449		
Gly	Gln	Leu	Leu	Asp	Tyr	Glu	Lys	Lys	Ile	Lys	Asn	Gln	Thr	Gly	Ala			
		290				295				300								
tca	ggg	cca	aag	agc	aaa	ctc	aag	ctg	ctg	cac	ctg	gag	aag	cca	aat	1497		
Ser	Gly	Pro	Lys	Ser	Lys	Leu	Lys	Leu	Leu	His	Leu	Glu	Lys	Pro	Asn			
305				310						315				320				
gaa	cct	gtc	cct	gct	gtc	tca	gag	ggt	gga	cag	aaa	agc	gag	acg	ccc	1545		
Glu	Pro	Val	Pro	Ala	Val	Ser	Glu	Gly	Gly	Gln	Lys	Ser	Glu	Thr	Pro			
				325				330						335				
ctc	agt	cca	ccc	tgt	gcc	gac	tct	gct	acc	tca	gag	gca	gca	gga	caa	1593		
Leu	Ser	Pro	Pro	Cys	Ala	Asp	Ser	Ala	Thr	Ser	Glu	Ala	Ala	Gly	Gln			
		340						345				350						
agg	ccc	gtg	cat	ccc	gcc	agc	gtg	ccc	agc	gtg	ccc	agc	gtg	cag	ccg	1641		
Arg	Pro	Val	His	Pro	Ala	Ser	Val	Pro	Ser	Val	Pro	Ser	Val	Gln	Pro			
		355				360				365								
tcg	ctg	tta	gag	gac	agc	ccg	ctg	gta	cag	gcg	ctc	agt	ggg	ctg	cac	1689		
Ser	Leu	Leu	Glu	Asp	Ser	Pro	Leu	Val	Gln	Ala	Leu	Ser	Gly	Leu	His			
		370				375				380								
ctg	tcc	gca	gac	agg	ctg	gaa	gac	agc	aat	aag	ctc	aag	cgt	tcc	ttc	1737		
Leu	Ser	Ala	Asp	Arg	Leu	Glu	Asp	Ser	Asn	Lys	Leu	Lys	Arg	Ser	Phe			
385				390						395		400						
tct	ctg	gat	atc	aaa	tca	gtt	tca	tat	tca	gcc	agc	atg	gca	gca	tcc	1785		
Ser	Leu	Asp	Ile	Lys	Ser	Val	Ser	Tyr	Ser	Ala	Ser	Met	Ala	Ala	Ser			
				405				410						415				
tta	cat	ggc	ttc	tcc	tca	tca	gaa	gat	gct	ttg	gaa	tac	tac	aaa	cct	1833		
Leu	His	Gly	Phe	Ser	Ser	Ser	Glu	Asp	Ala	Leu	Glu	Tyr	Tyr	Lys	Pro			
		420						425				430						
tcc	act	act	ctg	gat	ggg	acc	aac	aag	cta	tgc	cag	ttc	tcc	cct	gtt	1881		
Ser	Thr	Thr	Leu	Asp	Gly	Thr	Asn	Lys	Leu	Cys	Gln	Phe	Ser	Pro	Val			
		435				440				445								
cag	gaa	cta	tcg	gag	cag	act	ccc	gaa	acc	agt	cct	gat	aag	gag	gaa	1929		
Gln	Glu	Leu	Ser	Glu	Gln	Thr	Pro	Glu	Thr	Ser	Pro	Asp	Lys	Glu	Glu			
450						455				460								
gcc	agc	atc	ccc	aag	aag	ctg	cag	acc	gcc	agg	cct	tca	gac	agc	cag	1977		
Ala	Ser	Ile	Pro	Lys	Lys	Leu	Gln	Thr	Ala	Arg	Pro	Ser	Asp	Ser	Gln			
465				470				475		480								
agc	aag	cga	ttg	cat	tcg	gtc	aga	acc	agc	agc	agt	ggc	acc	gcc	cag	2025		
Ser	Lys	Arg	Leu	His	Ser	Val	Arg	Thr	Ser	Ser	Ser	Gly	Thr	Ala	Gln			
				485				490				495						
agg	tcc	ctt	tta	tct	cca	ctg	cat	cga	agt	ggg	agc	gtg	gag	gac	aat	2073		
Arg	Ser	Leu	Leu	Ser	Pro	Leu	His	Arg	Ser	Gly	Ser	Val	Glu	Asp	Asn			
		500						505				510						



ggggctttga ccactaccat atctggtagc ccattttcta ggcattgtga ataggttaggt 3212  
 agctagtcac acttttcaga ccaattcaaa ctgtctatgc acaaaattcc cgtgggccta 3272  
 gatggagata attttttttt cttctcagct ttatgaagag aagggaaact gtctaggatt 3332  
 cagctgaacc accaggaacc tggcaacatc acgatttaag ctaaggttgg gaggctaacg 3392  
 agtctacctc cctctttgta aatcaaagaa ttgtttaaaa tgggattgtc aatcctttaa 3452  
 ataaagatga acttggtttc aagccaaatg tgaatttatt tgggttggtg gcagagcagc 3512  
 agcaccttca aattctcagc caaagcagat gtttttgccc tttctgcttc actgcattga 3572  
 tacagttggt aaaatgtaat aatatggcag aattttatag gaaacttcct agggaggtaa 3632  
 attatgggaa gattaagaaa ggtacaaatt gctgaggaga agcaggaaac ctgtttcctt 3692  
 agtggctttt atcccctcgg catgcgatgg ggctgatgtt tctatgattg cctcagactt 3752  
 tcacatttac tagtagggct gagagaggct ttagtgagga aggaatattc agaataaaac 3812  
 ggttgagaaa gctgagaaga ccattgagtt ttgatcagtt gtgaatagag tgcaaagcca 3872  
 tggccaagct gtttttgaa acgctggccg gcgtgtcttc agtggaaaaa gcaaatacaa 3932  
 atggagcgag agcaaagggg cgtcctcagt cctcaacctc caatcactgt atggaatcgg 3992  
 tcctggcagc tgaacatagg aggtcactgg aacaagtgat agtgcagatt ggctttcaaa 4052  
 catectcctg gcttgagttt tatcagctac aatgtgggtc ctcttttgaa gccttaattc 4112  
 acaacagcag ctttttgagg gtggggctgg gcgggtgttg tcattgttct ttccttcctt 4172  
 gtaagtgtcg ctagttgctg cctcgatatc cagggttttc totgtttttg agaaatggac 4232  
 agttttttga ccaggatgtg acttcatgtt tcctatggtg acttctaaaa ccagcacaga 4292  
 atgatatgac tcaacacaga ccgacttggg tatggggatg atgagccgca cagacctcac 4352  
 tagttgtgca caaataatgt gctatgatgg ggtgtaaagt gaaggcagaa gagggtcagc 4412  
 cgcattgtta tgatactggg aaagtgtctg tcaacgattt gagttagttt ttagatatac 4472  
 attgaaatct ttaatcagac attctcaagt ttcacacagt agtttttgat gttatgtaca 4532  
 cacacaccaa atgtgtaaca gttcaccact tccagagtgt ggtcatgccc aaaacatgtt 4592  
 taagaaagga aagcagtagc tccttgctaa cgatgtttca ggagggtttg ggcacttggg 4652  
 tttaatgagc ttctgtcatt tagggcttct cttggccatg gtccccttcc ttctggaact 4712  
 gtgatgtagt cacatcctac agcctttagt gctgggtcac tagtgtcaga taatcagttc 4772  
 ttggaatcga gactgccgtg gcgaaggggt ggcctcggag gcaggctctg gagctgcttg 4832  
 gatgtcttta ggtgggggtg tggctggctc tcttcagcat gtaattgggg aaaccctcgc 4892  
 gtctactagg ggtgatacag atgggtgattt taaagagcaa aactagactt ctatgtgaga 4952  
 agtgctggaa aatgatttag gacatgtgta aagttagatg gaaagactgt aaatgtttaa 5012



tatgaatata gtgtttotitt gaagtaaggc cagctgttga acggttaaac tgtgcatttc 5072  
tcattttgat gtgtcatgta tgttaatgta tgaaatgatt aaataaaaatc aaaactggta 5132  
cctgtttata cataaatacg agaaaagacc tatcttttga gccataaact cgggtgggaac 5192  
accaccactc aagttgccaaggaggcagtggtgaaacct gtcctgtttct cacttaaatg 5252  
aggatttagc tcaaaataaaa gtgggtgggtgt catcagggttt attccgtgtt ctgtcattca 5312  
catggaacac cggatgatta gctaacagtt tagtgccagc cttcattctt tactgtgtac 5372  
gttaaatgca cactacagtg aaaaagccta agacacttgg taaatatttt ctagctgact 5432  
gattccagaa cacacaag 5450

<210> 148  
<211> 665  
<212> PRT  
<213> Homo sapiens

<400> 148

Met Ala His Glu Met Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
50 55 60

Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
65 70 75 80

Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
100 105 110

Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
 145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
 165 170 175

Lys Glu Leu Ile Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
 180 185 190

Tyr Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
 195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
 210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240

Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Asn Phe Asn Phe Leu  
 275 280 285

Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr Gly Ala  
 290 295 300

Ser Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn  
 305 310 315 320

Glu Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro  
 325 330 335

Leu Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln  
 340 345 350

Arg Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro  
 355 360 365

Ser Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His  
 370 375 380

Leu Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe

385

390

395

400

Ser Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser  
 405 410 415

Leu His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro  
 420 425 430

Ser Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val  
 435 440 445

Gln Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu  
 450 455 460

Ala Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln  
 465 470 475 480

Ser Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln  
 485 490 495

Arg Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn  
 500 505 510

Tyr His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu  
 515 520 525

Thr Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu  
 530 535 540

Ala Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala  
 545 550 555 560

Thr Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser  
 565 570 575

Ala Ser Tyr Ser Ala Tyr Ser Cys Ser Gln Leu Pro Thr Cys Gly Asp  
 580 585 590

Gln Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp  
 595 600 605

Ser Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys  
 610 615 620

Arg Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn  
 625 630 635 640

Arg Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser  
645 650 655

Gly Ser Met Glu Ile Ile Glu Val Ser  
660 665

<210> 149  
<211> 4393  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (628)..(2448)

<400> 149  
ccacgcgtcc ggctcttgcc tcccagtgcc atgcaggtgc aggatgcaac caggcggccc 60  
tcagccgtgc gcttcctcag ctcccttctc cagggccgcc ggcactccac ctccagacca 120  
gtactgcggc tgcagcaggc ccggcggggc tctggcttgg gctccggctc tgccacgaag 180  
ctgctgtcct cgtcctctct ccagtgatg gtggctgttt cctcagtcag ccattgcagag 240  
ggaaacccaa ctttccccga aagaaaaaga aatttagaac gtccaacacc aaagtacaca 300  
aaagtagggg agcggttacg gcatgtcatt cctggacaca tggcatgttc catggcgtgt 360  
ggcggtagag cttgcaagta tgagaaccca gcccgctgga gtgagcagga gcaagccatt 420  
aaggggggttt actcatcctg ggtcactgat aatatactgg ccattggcccg cccatcctct 480  
gagctcctgg agaagtacca catcattgat cagttcctca gccatggcat aaaaacaata 540  
atcaacctcc agcgccctgg tgagcatgct agctgtggga accctctgga acaagaaagt 600  
ggcttcacat accttctga ggctttc atg gag gct ggc att tac ttc tac aat 654  
Met Glu Ala Gly Ile Tyr Phe Tyr Asn  
1 5  
ttc gga tgg aag gat tat ggt gta gcg tct ctt act act atc cta gat 702  
Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu Thr Thr Ile Leu Asp  
10 15 20 25  
atg gtg aag gtg atg aca ttt gcc tta cag gaa gga aaa gta gct atc 750  
Met Val Lys Val Met Thr Phe Ala Leu Gln Glu Gly Lys Val Ala Ile  
30 35 40  
cat tgt cat gca ggg ctt ggt cga aca ggt gtt tta ata gcc tgt tac 798  
His Cys His Ala Gly Leu Gly Arg Thr Gly Val Leu Ile Ala Cys Tyr  
45 50 55  
tta gtt ttt gca acg aga atg act gct gac caa gca att ata ttt gtg 846  
Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln Ala Ile Ile Phe Val  
60 65 70  
cgg gca aag cga ccc aat tcc ata caa acc aga gga cag ctc ctc tgt 894

Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg	Gly	Gln	Leu	Leu	Cys	
75						80					85					
gta	agg	gaa	ttt	act	cag	ttt	cta	act	cct	ctc	cgc	aat	ata	ttc	tct	942
Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu	Arg	Asn	Ile	Phe	Ser	
90					95					100					105	
tgc	tgt	gat	ccc	aaa	gca	cat	gct	gtc	acc	tta	cct	caa	tat	cta	att	990
Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu	Pro	Gln	Tyr	Leu	Ile	
				110					115					120		
cgc	cag	cgt	cat	ctg	ctt	cat	ggc	tat	gag	gca	cga	ctt	ctg	aaa	cac	1038
Arg	Gln	Arg	His	Leu	Leu	His	Gly	Tyr	Glu	Ala	Arg	Leu	Leu	Lys	His	
			125					130					135			
gtg	cca	aaa	att	atc	cac	cta	gtt	tgc	aaa	ttg	ctg	ctg	gac	tta	gcg	1086
Val	Pro	Lys	Ile	Ile	His	Leu	Val	Cys	Lys	Leu	Leu	Leu	Asp	Leu	Ala	
		140					145					150				
gag	aac	agg	cca	gtg	atg	atg	aag	gat	gtg	tcc	gaa	gga	cct	ggc	ctc	1134
Glu	Asn	Arg	Pro	Val	Met	Met	Lys	Asp	Val	Ser	Glu	Gly	Pro	Gly	Leu	
	155					160					165					
tct	gct	gaa	ata	gaa	aag	aca	atg	tct	gag	atg	gtc	acc	atg	cag	ctg	1182
Ser	Ala	Glu	Ile	Glu	Lys	Thr	Met	Ser	Glu	Met	Val	Thr	Met	Gln	Leu	
170					175					180					185	
gat	aaa	gag	tta	ctg	agg	cat	gac	agt	gat	gtg	tcc	aac	ccg	cct	aac	1230
Asp	Lys	Glu	Leu	Leu	Arg	His	Asp	Ser	Asp	Val	Ser	Asn	Pro	Pro	Asn	
				190					195					200		
ccc	act	gca	gtg	gca	gca	gat	ttt	gac	aat	cga	ggc	atg	att	ttc	tcc	1278
Pro	Thr	Ala	Val	Ala	Ala	Asp	Phe	Asp	Asn	Arg	Gly	Met	Ile	Phe	Ser	
			205					210					215			
aat	gag	caa	cag	ttt	gac	cct	ctt	tgg	aaa	agg	cgg	aat	gtt	gag	tgc	1326
Asn	Glu	Gln	Gln	Phe	Asp	Pro	Leu	Trp	Lys	Arg	Arg	Asn	Val	Glu	Cys	
		220					225					230				
ctt	caa	ccc	ctg	act	cat	ctg	aaa	agg	cgg	ctc	agc	tac	agt	gac	tca	1374
Leu	Gln	Pro	Leu	Thr	His	Leu	Lys	Arg	Arg	Leu	Ser	Tyr	Ser	Asp	Ser	
	235					240					245					
gat	tta	aag	agg	gcc	gag	aac	ctc	ctg	gag	caa	ggg	gag	act	cca	cag	1422
Asp	Leu	Lys	Arg	Ala	Glu	Asn	Leu	Leu	Glu	Gln	Gly	Glu	Thr	Pro	Gln	
250					255				260						265	
aca	gtg	cct	gcc	cag	atc	ttg	gtt	ggc	cac	aag	ccc	agg	cag	cag	aag	1470
Thr	Val	Pro	Ala	Gln	Ile	Leu	Val	Gly	His	Lys	Pro	Arg	Gln	Gln	Lys	
				270				275						280		
ctc	ata	agc	cat	tgt	tac	atc	cca	cag	tct	cca	gaa	cca	gac	tta	cac	1518
Leu	Ile	Ser	His	Cys	Tyr	Ile	Pro	Gln	Ser	Pro	Glu	Pro	Asp	Leu	His	
			285					290					295			
aag	gaa	gcc	ttg	gtt	cgc	agc	aca	ctt	tct	ttc	tgg	agt	cag	tca	aag	1566
Lys	Glu	Ala	Leu	Val	Arg	Ser	Thr	Leu	Ser	Phe	Trp	Ser	Gln	Ser	Lys	
		300					305					310				
ttt	gga	ggc	ctg	gaa	gga	ctc	aaa	gat	aat	ggg	tca	cca	att	ttc	cat	1614
Phe	Gly	Gly	Leu	Glu	Gly	Leu	Lys	Asp	Asn	Gly	Ser	Pro	Ile	Phe	His	



gtt aat ttt gat tot gaa aat gga cca aca gtt tac aac acc ctg aag	2382
Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Leu Lys	
570 575 580 585	
aaa ata ttt aag cac acg ctg gaa gaa aaa aga aaa atg aca aaa gat	2430
Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp	
590 595 600	
ggc cct aag cct ggc ctc tagctttcac tcatgggtgaa tatttcagac	2478
Gly Pro Lys Pro Gly Leu	
605	
ctaaagatcc agatagtatc tctgttcata tgtgaataag ttgaagattg tggggctact	2538
ttttctcata gcactttatt ttgaatgttg ttagtttgtg ctgagaatgg tcgtccgtat	2598
ttgaaccaat tatttatttt aaaatatatt taagctacat ttttgttttg aaaaattgcc	2658
ataaatttgg tgccactttc ttttatttat ttgactgagt taatattatt gtattaacat	2718
tttaagtata tgggtgtttac attcttattt cttttgacat tttggaaata atcataactt	2778
gtctttccaa aataaccatt ttcttgatgg aactcttctc agagttttta ccaaatagct	2838
aacttttagta gtaaaacctc attgtgtatc cattccccca cagatgaact aagaaagtca	2898
ccaagtgtct taagctgttt tatatttggt acgaagaagg ctattgctac aatattttta	2958
aaggtttctt ttttaacttt gaaatttttt gtttttctt ttctttttat aaatgtaaca	3018
gagggtttca aagcatatta tttttcagag agatttagtt ttactttaat ggagtgactg	3078
tgaagtgggt gggatttttt gcttgtagaa agtagacttg ctctttgtca gattttccaaa	3138
caaccttgcc agccttggtt gtcaaaagga ggcaggagca gttctcaaca caccaagcct	3198
tattcccact cccttggtt gctgctgagc caaatagcat ctttacagag gaagtgggat	3258
cagaggcagg aagtgtggaa agttgctaag aagcagggtt tgccctctgtc ctcccgggga	3318
ctccacaggg atattcgtgc agggcagggg ctctgtgccg gccctgctct ctccagatgcc	3378
acagccactc tgcagagggt actcttgagg ctggagggaag tcaaaaactgg gccactgttt	3438
gtactgatgg tgtattagca tgagcagcgt ggccctggcc ccacactccc aaatctgcc	3498
ctccatagac ccacttgcc caaggcttta tatttggttg ctttcttaca atgagaatta	3558
agatttttaa actgaagttg accatacagg ttgcattagc cctaactggc ttcatgtaag	3618
aagggtgact gcctaaacta gttccttgta agctgaacca tcaattatca gttgaagcca	3678
tacttttatt taaattaata tacgtagata ccagaggcca agccacagag aggataatag	3738
ttcttcccaa taaaggatgat attaatacaga ctaatttcga actaaagaag ttactgctta	3798
aagacggaat ttccagggga gcaagactca tttagaacia atgaaatttc tccagtccta	3858
catttctgaa ttgacttcta gcacatcaaa aatatttcag tcattatcag tctcattaac	3918

tgaaatgcc aatgctaaat gcagtgttct ttcacactgt ttttaattttc ttgggaaatt 3978  
 gagtccagtg gatgttaatg gagtgggttg cccatccctg aaatgtctta ttttcaagtg 4038  
 cctggcctgg gaaagaaggg gaagaaacaa ttgcattata tccaaagata cactataaaa 4098  
 atagagtttt taccaaaaaa agatgtttgt tctcatctca gtaggcctca tttgggcaag 4158  
 tgacccacag gtcttttggc gagtttgcta tttgcctggt gaaatacttg tttcaactta 4218  
 gagaacagtt atgatgtgac catagcatgg cacaactaaa aatctaagcc tgaaacctga 4278  
 aaaaagagat atgacaaggg aaattaatca ggctatacat aagtattgta tttatttgaa 4338  
 taaaaataaa aagagcaacc cataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaag 4393

<210> 150  
 <211> 607  
 <212> PRT  
 <213> Homo sapiens

<400> 150

Met Glu Ala Gly Ile Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly  
 1 5 10 15

Val Ala Ser Leu Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe  
 20 25 30

Ala Leu Gln Glu Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly  
 35 40 45

Arg Thr Gly Val Leu Ile Ala Cys Tyr Leu Val Phe Ala Thr Arg Met  
 50 55 60

Thr Ala Asp Gln Ala Ile Ile Phe Val Arg Ala Lys Arg Pro Asn Ser  
 65 70 75 80

Ile Gln Thr Arg Gly Gln Leu Leu Cys Val Arg Glu Phe Thr Gln Phe  
 85 90 95

Leu Thr Pro Leu Arg Asn Ile Phe Ser Cys Cys Asp Pro Lys Ala His  
 100 105 110

Ala Val Thr Leu Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His  
 115 120 125

Gly Tyr Glu Ala Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu  
 130 135 140

Val Cys Lys Leu Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met





Pro Leu Asp Cys Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His  
 405 410 415

Glu Thr Gln Asp Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala  
 420 425 430

Leu Gln Ser Glu Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys  
 435 440 445

Ala Leu Ala Asn Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg  
 450 455 460

Lys Val Glu Met Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp  
 465 470 475 480

Glu Arg Ile Cys Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met  
 485 490 495

Trp Ser Trp Val Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp  
 500 505 510

Val Asp Met Leu Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe  
 515 520 525

Leu Leu Glu Lys Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys  
 530 535 540

Ile Val Asn Leu Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu  
 545 550 555 560

Ala His Ala Ile Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn  
 565 570 575

Gly Pro Thr Val Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu  
 580 585 590

Glu Glu Lys Arg Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu  
 595 600 605

<210> 151  
 <211> 878  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS

<222> (89)..(538)

<400> 151

ccacgcgtcc ggcgagggga cgcgtgggcg gagcggggct ggccagcctc ggcccccatg 60

accgcgtgtc ctgtgccctt tcccagcg atg ggc gtg cag ccc ccc aac ttc 112

Met Gly Val Gln Pro Pro Asn Phe  
1 5

tcc tgg gtg ctt ccg ggc cgg ctg gcg gga ctg gcg ctg ccg cgg ctc 160

Ser Trp Val Leu Pro Gly Arg Leu Ala Gly Leu Ala Leu Pro Arg Leu  
10 15 20

ccc gcc cac tac cag ttc ctg ttg gac ctg ggc gtg cgg cac ctg gtg 208

Pro Ala His Tyr Gln Phe Leu Leu Asp Leu Gly Val Arg His Leu Val  
25 30 35 40

tcc ctg acg gag cgc ggg ccc cct cac agc gac agc tgc ccc ggc ctc 256

Ser Leu Thr Glu Arg Gly Pro Pro His Ser Asp Ser Cys Pro Gly Leu  
45 50 55

acc ctg cac cgc ctg cgc atc ccc gac ttc tgc ccg ccg gcc ccc gac 304

Thr Leu His Arg Leu Arg Ile Pro Asp Phe Cys Pro Pro Ala Pro Asp  
60 65 70

cag atc gac cgc ttc gtg cag atc gtg gac gag gcc aac gca cgg gga 352

Gln Ile Asp Arg Phe Val Gln Ile Val Asp Glu Ala Asn Ala Arg Gly  
75 80 85

gag gct gtg gga gtg cac tgt gct ctg ggc ttt ggc cgc act ggc acc 400

Glu Ala Val Gly Val His Cys Ala Leu Gly Phe Gly Arg Thr Gly Thr  
90 95 100

atg ctg gcc tgt tac ctg gtg aag gag cgg ggc ttg gct gca gga gat 448

Met Leu Ala Cys Tyr Leu Val Lys Glu Arg Gly Leu Ala Ala Gly Asp  
105 110 115 120

gcc att gct gaa atc cga cga cta cga ccc ggc tcc atc gag acc tat 496

Ala Ile Ala Glu Ile Arg Arg Leu Arg Pro Gly Ser Ile Glu Thr Tyr  
125 130 135

gag cag gag aaa gca gtc ttc cag ttc tac cag cga acg aaa 538

Glu Gln Glu Lys Ala Val Phe Gln Phe Tyr Gln Arg Thr Lys  
140 145 150

taaggggcct tagtaccctt ctaccaggcc ctcaactcccc ttcccatgt tgtcgatggg 598

gccagagatg aagggaagtg gactaaagta ttaaaccctc tagctcccat tggctgaaga 658

cactgaagta gcccaccctt gcaggcaggt cctgattgaa ggggaggctt gtactgcttt 718

gttgaataaaa tgagtttttac gaaccaggaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 778

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 838

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc 878

<210> 152

<211> 150

<212> PRT

<213> Homo sapiens

<400> 152

Met Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu  
1 5 10 15

Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu  
20 25 30

Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro  
35 40 45

His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro  
50 55 60

Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile  
65 70 75 80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala  
85 90 95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys  
100 105 110

Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu  
115 120 125

Arg Pro Gly Ser Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln  
130 135 140

Phe Tyr Gln Arg Thr Lys  
145 150

<210> 153

<211> 470

<212> PRT

<213> Homo sapiens

<400> 153

Met Glu Ala Gly Ile Tyr Phe Asn Phe Gly Trp Lys Asp Tyr Gly Val  
1 5 10 15

Ala Ser Leu Thr Thr Ile Asp Met Val Lys Val Met Thr Phe Ala Leu  
20 25 30

Gln Glu Gly Lys Val Ile His Cys His Ala Gly Leu Gly Arg Thr Gly  
35 40 45

Val Leu Ile Ala Tyr Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln

50					55					60					
Ala 65	Ile	Ile	Val	Arg	Ala 70	Lys	Arg	Pro	Asn	Ser 75	Ile	Gln	Thr	Arg	Gly 80
Gln	Leu	Cys	Val	Arg 85	Glu	Phe	Thr	Gln	Phe 90	Leu	Thr	Pro	Leu	Arg 95	Asn
Ile	Ser	Cys	Cys 100	Asp	Pro	Lys	Ala	His 105	Ala	Val	Thr	Leu	Pro 110	Gln	Tyr
Ile	Arg	Gln 115	Arg	His	Leu	Leu	His 120	Gly	Tyr	Glu	Ala	Arg 125	Leu	Leu	His
Val	Pro 130	Lys	Ile	Ile	His	Leu 135	Val	Cys	Lys	Leu	Leu 140	Leu	Asp	Ala	Glu
Asn 145	Arg	Pro	Val	Met	Met 150	Lys	Asp	Val	Ser	Glu 155	Gly	Pro	Leu	Ser	Ala 160
Glu	Ile	Glu	Lys	Thr 165	Met	Ser	Glu	Met	Val 170	Thr	Met	Leu	Asp	Lys	Glu 175
Leu	Leu	Arg	His 180	Asp	Ser	Asp	Val	Ser 185	Asn	Pro	Asn	Pro	Thr	Ala	Val
Ala	Ala 195	Asp	Phe	Asp	Asn	Arg	Gly 200	Met	Ile	Ser	Asn	Glu 205	Gln	Gln	Phe
Asp	Pro 210	Leu	Trp	Lys	Arg	Arg 215	Asn	Val	Cys	Leu	Gln 220	Pro	Leu	Thr	His
Leu 225	Lys	Arg	Arg	Leu	Ser 230	Tyr	Ser	Ser	Asp	Leu 235	Lys	Arg	Ala	Glu	Asn 240
Leu	Leu	Glu	Gln	Gly 245	Glu	Thr	Gln	Thr	Val 250	Pro	Ala	Gln	Ile	Leu	Val 255
Gly	His	Lys	Pro 260	Arg	Gln	Lys	Leu	Ile	Ser	His	Cys	Tyr	Ile	Pro	Gln
Ser	Pro 275	Glu	Pro	Asp	His	Lys	Glu 280	Ala	Leu	Val	Arg	Ser 285	Thr	Leu	Ser
Phe	Trp 290	Ser	Gln	Lys	Phe	Gly 295	Gly	Leu	Glu	Gly	Leu 300	Lys	Asp	Asn	Gly
Ser 305	Pro	Ile	His	Gly	Arg 310	Ile	Ile	Pro	Lys	Glu 315	Ala	Gln	Gln	Ser	Gly 320
Ala	Phe	Ala	Asp	Val 325	Ser	Gly	Ser	His	Ser 330	Pro	Gly	Glu	Pro	Val 335	Ser
Pro	Phe	Ala	Asn 340	Val	His	Lys	Asp	Pro 345	Asn	Pro	Ala	His	Gln	Gln	Val
His	Cys	Gln 355	Cys	Lys	Thr	His	Gly 360	Val	Gly	Ser	Pro	Gly 365	Ser	Val	Gln
Asn	Ser 370	Arg	Thr	Pro	Arg	Ser 375	Pro	Leu	Asp	Cys	Gly 380	Ser	Ser	Lys	Ala

Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Ser Glu Ala  
385 390 395 400

Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Ala Arg Arg Ile  
405 410 415

Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Val Glu Lys Glu Glu  
420 425 430

Leu Lys Arg Lys Val Glu Met Trp Gln Lys Leu Asn Ser Arg Asp Gly  
435 440 445

Ala Trp Glu Arg Ile Cys Gly Glu Arg Pro Phe Ile Leu Cys Ser Leu  
450 455 460

Met Trp Ser Trp Val Glu  
465 470

<210> 154  
<211> 24  
<212> DNA  
<213> Homo sapiens  
  
<400> 154  
tacaatttcg gatggaagga ttat

24

<210> 155  
<211> 23  
<212> DNA  
<213> Homo sapiens  
  
<400> 155  
gcatgacaat ggatagctac ttt

23

<210> 156  
<211> 24  
<212> DNA  
<213> Homo sapiens  
  
<400> 156  
gagaaagcag tcttcagtt ctac

24

<210> 157  
<211> 24  
<212> DNA  
<213> Homo sapiens  
  
<400> 157  
atgggagcta gagggtttaa tact

24

<210> 158  
<211> 14  
<212> PRT  
<213> Homo sapiens  
  
<400> 158



[illegible]

```
<210> 165
<211> 13
<212> PRT
<213> Homo sapiens
```

```
<210> 166
<211> 23
<212> PRT
<213> Homo sapiens
```

```
<210> 167
<211> 39
<212> DNA
<213> Homo sapiens
```

```
<210> 168
<211> 33
<212> DNA
<213> Homo sapiens
```

```
<210> 169
<211> 38
<212> DNA
<213> Homo sapiens
```

```
<210> 170
<211> 35
<212> DNA
<213> Homo sapiens
```



<400> 170  
gcagcagtcg accacccaag accacatcaa gctgc 35

<210> 171  
<211> 39  
<212> DNA  
<213> Homo sapiens

<400> 171  
gcagcagcgg ccgcctgttg gacctgggcg tgcggcacc 39

<210> 172  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 172  
gcagcagtcg actttcgttc gctggtagaa ctggaag 37

<210> 173  
<211> 38  
<212> DNA  
<213> Homo sapiens

<400> 173  
gcagcagcgg ccgcatgggc gtgcagcccc ccaacttc 38

<210> 174  
<211> 37  
<212> DNA  
<213> Homo sapiens

<400> 174  
gcagcagtcg accaccaggt aacaggccag catggtg 37

<210> 175  
<211> 806  
<212> PRT  
<213> Homo sapiens

<400> 175

Met Gln Val Gln Asp Ala Thr Arg Arg Pro Ser Ala Val Arg Phe Leu  
1 5 10 15

Ser Ser Phe Leu Gln Gly Arg Arg His Ser Thr Ser Asp Pro Val Leu  
20 25 30

Arg Leu Gln Gln Ala Arg Arg Gly Ser Gly Leu Gly Ser Gly Ser Ala  
35 40 45

Thr Lys Leu Leu Ser Ser Ser Ser Leu Gln Val Met Val Ala Val Ser  
50 55 60

Ser Val Ser His Ala Glu Gly Asn Pro Thr Phe Pro Glu Arg Lys Arg  
65 70 75 80

Asn	Leu	Glu	Arg	Pro	Thr	Pro	Lys	Tyr	Thr	Lys	Val	Gly	Glu	Arg	Leu		
				85					90					95			
Arg	His	Val	Ile	Pro	Gly	His	Met	Ala	Cys	Ser	Met	Ala	Cys	Gly	Gly		
			100					105						110			
Arg	Ala	Cys	Lys	Tyr	Glu	Asn	Pro	Ala	Arg	Trp	Ser	Glu	Gln	Glu	Gln		
		115					120					125					
Ala	Ile	Lys	Gly	Val	Tyr	Ser	Ser	Trp	Val	Thr	Asp	Asn	Ile	Leu	Ala		
	130					135					140						
Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	Tyr	His	Ile	Ile	Asp		
145					150					155					160		
Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	Asn	Leu	Gln	Arg	Pro		
				165					170					175			
Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	Gln	Glu	Ser	Gly	Phe		
			180					185					190				
Thr	Tyr	Leu	Pro	Glu	Ala	Phe	Met	Glu	Ala	Gly	Ile	Tyr	Phe	Tyr	Asn		
		195					200						205				
Phe	Gly	Trp	Lys	Asp	Tyr	Gly	Val	Ala	Ser	Leu	Thr	Thr	Ile	Leu	Asp		
	210					215					220						
Met	Val	Lys	Val	Met	Thr	Phe	Ala	Leu	Gln	Glu	Gly	Lys	Val	Ala	Ile		
225					230					235					240		
His	Cys	His	Ala	Gly	Leu	Gly	Arg	Thr	Gly	Val	Leu	Ile	Ala	Cys	Tyr		
				245					250					255			
Leu	Val	Phe	Ala	Thr	Arg	Met	Thr	Ala	Asp	Gln	Ala	Ile	Ile	Phe	Val		
			260					265					270				
Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg	Gly	Gln	Leu	Leu	Cys		
		275					280					285					
Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu	Arg	Asn	Ile	Phe	Ser		
		290				295					300						
Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu	Pro	Gln	Tyr	Leu	Ile		
305					310					315					320		
Arg	Gln	Arg	His	Leu	Leu	His	Gly	Tyr	Glu	Ala	Arg	Leu	Leu	Lys	His		
				325					330					335			
Val	Pro	Lys	Ile	Ile	His	Leu	Val	Cys	Lys	Leu	Leu	Leu	Asp	Leu	Ala		
			340					345					350				
Glu	Asn	Arg	Pro	Val	Met	Met	Lys	Asp	Val	Ser	Glu	Gly	Pro	Gly	Leu		
		355					360					365					
Ser	Ala	Glu	Ile	Glu	Lys	Thr	Met	Ser	Glu	Met	Val	Thr	Met	Gln	Leu		
		370				375					380						
Asp	Lys	Glu	Leu	Leu	Arg	His	Asp	Ser	Asp	Val	Ser	Asn	Pro	Pro	Asn		
385					390				395						400		

Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg Gly Met Ile Phe Ser  
 405 410 415  
 Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg Arg Asn Val Glu Cys  
 420 425 430  
 Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu Ser Tyr Ser Asp Ser  
 435 440 445  
 Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln Gly Glu Thr Pro Gln  
 450 455 460  
 Thr Val Pro Ala Gln Ile Leu Val Gly His Lys Pro Arg Gln Gln Lys  
 465 470 475 480  
 Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro Glu Pro Asp Leu His  
 485 490 495  
 Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe Trp Ser Gln Ser Lys  
 500 505 510  
 Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly Ser Pro Ile Phe His  
 515 520 525  
 Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser Gly Ala Phe Ser Ala  
 530 535 540  
 Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro Val Ser Pro Ser Phe  
 545 550 555 560  
 Ala Asn Val His Lys Asp Pro Asn Pro Ala His Gln Gln Val Ser His  
 565 570 575  
 Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro Gly Ser Val Arg Gln  
 580 585 590  
 Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys Gly Ser Ser Pro Lys  
 595 600 605  
 Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp Ser Lys Asp Leu Ser  
 610 615 620  
 Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu Leu Ser Ala Glu Ala  
 625 630 635 640  
 Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn Leu Asn Glu Ser Val  
 645 650 655  
 Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met Trp Gln Lys Glu Leu  
 660 665 670  
 Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys Gly Glu Arg Asp Pro  
 675 680 685  
 Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val Glu Gln Leu Lys Glu  
 690 695 700  
 Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu Val Asp Arg Arg Ala  
 705 710 715 720  
 Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys Gly Gln His Gln Thr



195					200					205					
Ala	Ile	Ile	Phe	Val	Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg
210						215					220				
Gly	Gln	Leu	Leu	Cys	Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu
225					230					235				240	
Arg	Asn	Ile	Phe	Ser	Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu
				245					250					255	
Pro	Gln	Tyr	Leu	Ile	Arg	Gln	Arg	His	Leu	Leu	His	Gly	Tyr	Glu	Ala
			260					265						270	
Arg	Leu	Leu	Lys	His	Val	Pro	Lys	Ile	Ile	His	Leu	Val	Cys	Lys	Leu
			275				280					285			
Leu	Leu	Asp	Leu	Ala	Glu	Asn	Arg	Pro	Val	Met	Met	Lys	Asp	Val	Ser
		290					295					300			
Glu	Gly	Pro	Gly	Leu	Ser	Ala	Glu	Ile	Glu	Lys	Thr	Met	Ser	Glu	Met
305					310					315				320	
Val	Thr	Met	Gln	Leu	Asp	Lys	Glu	Leu	Leu	Arg	His	Asp	Ser	Asp	Val
			325						330					335	
Ser	Asn	Pro	Pro	Asn	Pro	Thr	Ala	Val	Ala	Ala	Asp	Phe	Asp	Asn	Arg
			340					345					350		
Gly	Met	Ile	Phe	Ser	Asn	Glu	Gln	Gln	Phe	Asp	Pro	Leu	Trp	Lys	Arg
		355					360					365			
Arg	Asn	Val	Glu	Cys	Leu	Gln	Pro	Leu	Thr	His	Leu	Lys	Arg	Arg	Leu
		370				375					380				
Ser	Tyr	Ser	Asp	Ser	Asp	Leu	Lys	Arg	Ala	Glu	Asn	Leu	Leu	Glu	Gln
385					390					395				400	
Gly	Glu	Thr	Pro	Gln	Thr	Val	Pro	Ala	Gln	Ile	Leu	Val	Gly	His	Lys
				405					410					415	
Pro	Arg	Gln	Gln	Lys	Leu	Ile	Ser	His	Cys	Tyr	Ile	Pro	Gln	Ser	Pro
			420					425					430		
Glu	Pro	Asp	Leu	His	Lys	Glu	Ala	Leu	Val	Arg	Ser	Thr	Leu	Ser	Phe
		435					440					445			
Trp	Ser	Gln	Ser	Lys	Phe	Gly	Gly	Leu	Glu	Gly	Leu	Lys	Asp	Asn	Gly
		450				455					460				
Ser	Pro	Ile	Phe	His	Gly	Arg	Ile	Ile	Pro	Lys	Glu	Ala	Gln	Gln	Ser
465					470					475				480	
Gly	Ala	Phe	Ser	Ala	Asp	Val	Ser	Gly	Ser	His	Ser	Pro	Gly	Glu	Pro
				485				490						495	
Val	Ser	Pro	Ser	Phe	Ala	Asn	Val	His	Lys	Asp	Pro	Asn	Pro	Ala	His
			500					505					510		
Gln	Gln	Val	Ser	His	Cys	Gln	Cys	Lys	Thr	His	Gly	Val	Gly	Ser	Pro
		515					520					525			

Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys  
530 535 540

Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp  
545 550 555 560

Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu  
565 570 575

Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn  
580 585 590

Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met  
595 600 605

Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys  
610 615 620

Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val  
625 630 635 640

Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu  
645 650 655

Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys  
660 665 670

Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys Ile Val Asn Leu  
675 680 685

Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile  
690 695 700

Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val  
705 710 715 720

Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg  
725 730 735

Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu  
740 745

<210> 177  
<211> 699  
<212> PRT  
<213> Homo sapiens  
  
<400> 177

Met Ala Cys Gly Gly Arg Ala Cys Lys Tyr Glu Asn Pro Ala Arg Trp  
1 5 10 15

Ser Glu Gln Glu Gln Ala Ile Lys Gly Val Tyr Ser Ser Trp Val Thr  
20 25 30

Asp Asn Ile Leu Ala Met Ala Arg Pro Ser Ser Glu Leu Leu Glu Lys  
35 40 45

Tyr His Ile Ile Asp Gln Phe Leu Ser His Gly Ile Lys Thr Ile Ile  
50 55 60

Asn Leu Gln Arg Pro Gly Glu His Ala Ser Cys Gly Asn Pro Leu Glu  
 65 70 75 80  
 Gln Glu Ser Gly Phe Thr Tyr Leu Pro Glu Ala Phe Met Glu Ala Gly  
 85 90 95  
 Ile Tyr Phe Tyr Asn Phe Gly Trp Lys Asp Tyr Gly Val Ala Ser Leu  
 100 105 110  
 Thr Thr Ile Leu Asp Met Val Lys Val Met Thr Phe Ala Leu Gln Glu  
 115 120 125  
 Gly Lys Val Ala Ile His Cys His Ala Gly Leu Gly Arg Thr Gly Val  
 130 135 140  
 Leu Ile Ala Cys Tyr Leu Val Phe Ala Thr Arg Met Thr Ala Asp Gln  
 145 150 155 160  
 Ala Ile Ile Phe Val Arg Ala Lys Arg Pro Asn Ser Ile Gln Thr Arg  
 165 170 175  
 Gly Gln Leu Leu Cys Val Arg Glu Phe Thr Gln Phe Leu Thr Pro Leu  
 180 185 190  
 Arg Asn Ile Phe Ser Cys Cys Asp Pro Lys Ala His Ala Val Thr Leu  
 195 200 205  
 Pro Gln Tyr Leu Ile Arg Gln Arg His Leu Leu His Gly Tyr Glu Ala  
 210 215 220  
 Arg Leu Leu Lys His Val Pro Lys Ile Ile His Leu Val Cys Lys Leu  
 225 230 235 240  
 Leu Leu Asp Leu Ala Glu Asn Arg Pro Val Met Met Lys Asp Val Ser  
 245 250 255  
 Glu Gly Pro Gly Leu Ser Ala Glu Ile Glu Lys Thr Met Ser Glu Met  
 260 265 270  
 Val Thr Met Gln Leu Asp Lys Glu Leu Leu Arg His Asp Ser Asp Val  
 275 280 285  
 Ser Asn Pro Pro Asn Pro Thr Ala Val Ala Ala Asp Phe Asp Asn Arg  
 290 295 300  
 Gly Met Ile Phe Ser Asn Glu Gln Gln Phe Asp Pro Leu Trp Lys Arg  
 305 310 315 320  
 Arg Asn Val Glu Cys Leu Gln Pro Leu Thr His Leu Lys Arg Arg Leu  
 325 330 335  
 Ser Tyr Ser Asp Ser Asp Leu Lys Arg Ala Glu Asn Leu Leu Glu Gln  
 340 345 350  
 Gly Glu Thr Pro Gln Thr Val Pro Ala Gln Ile Leu Val Gly His Lys  
 355 360 365  
 Pro Arg Gln Gln Lys Leu Ile Ser His Cys Tyr Ile Pro Gln Ser Pro  
 370 375 380

Glu Pro Asp Leu His Lys Glu Ala Leu Val Arg Ser Thr Leu Ser Phe  
 385 390 395 400  
 Trp Ser Gln Ser Lys Phe Gly Gly Leu Glu Gly Leu Lys Asp Asn Gly  
 405 410 415  
 Ser Pro Ile Phe His Gly Arg Ile Ile Pro Lys Glu Ala Gln Gln Ser  
 420 425 430  
 Gly Ala Phe Ser Ala Asp Val Ser Gly Ser His Ser Pro Gly Glu Pro  
 435 440 445  
 Val Ser Pro Ser Phe Ala Asn Val His Lys Asp Pro Asn Pro Ala His  
 450 455 460  
 Gln Gln Val Ser His Cys Gln Cys Lys Thr His Gly Val Gly Ser Pro  
 465 470 475 480  
 Gly Ser Val Arg Gln Asn Ser Arg Thr Pro Arg Ser Pro Leu Asp Cys  
 485 490 495  
 Gly Ser Ser Pro Lys Ala Gln Phe Leu Val Glu His Glu Thr Gln Asp  
 500 505 510  
 Ser Lys Asp Leu Ser Glu Ala Ala Ser His Ser Ala Leu Gln Ser Glu  
 515 520 525  
 Leu Ser Ala Glu Ala Arg Arg Ile Leu Ala Ala Lys Ala Leu Ala Asn  
 530 535 540  
 Leu Asn Glu Ser Val Glu Lys Glu Glu Leu Lys Arg Lys Val Glu Met  
 545 550 555 560  
 Trp Gln Lys Glu Leu Asn Ser Arg Asp Gly Ala Trp Glu Arg Ile Cys  
 565 570 575  
 Gly Glu Arg Asp Pro Phe Ile Leu Cys Ser Leu Met Trp Ser Trp Val  
 580 585 590  
 Glu Gln Leu Lys Glu Pro Val Ile Thr Lys Glu Asp Val Asp Met Leu  
 595 600 605  
 Val Asp Arg Arg Ala Asp Ala Ala Glu Ala Leu Phe Leu Leu Glu Lys  
 610 615 620  
 Gly Gln His Gln Thr Ile Leu Cys Val Leu His Cys Ile Val Asn Leu  
 625 630 635 640  
 Gln Thr Ile Pro Val Asp Val Glu Glu Ala Phe Leu Ala His Ala Ile  
 645 650 655  
 Lys Ala Phe Thr Lys Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val  
 660 665 670  
 Tyr Asn Thr Leu Lys Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg  
 675 680 685  
 Lys Met Thr Lys Asp Gly Pro Lys Pro Gly Leu  
 690 695

<210> 178



<211> 662  
 <212> PRT  
 <213> Homo sapiens

<400> 178

Met	Ala	Arg	Pro	Ser	Ser	Glu	Leu	Leu	Glu	Lys	Tyr	His	Ile	Ile	Asp
1				5					10					15	
Gln	Phe	Leu	Ser	His	Gly	Ile	Lys	Thr	Ile	Ile	Asn	Leu	Gln	Arg	Pro
			20					25					30		
Gly	Glu	His	Ala	Ser	Cys	Gly	Asn	Pro	Leu	Glu	Gln	Glu	Ser	Gly	Phe
		35					40					45			
Thr	Tyr	Leu	Pro	Glu	Ala	Phe	Met	Glu	Ala	Gly	Ile	Tyr	Phe	Tyr	Asn
	50					55					60				
Phe	Gly	Trp	Lys	Asp	Tyr	Gly	Val	Ala	Ser	Leu	Thr	Thr	Ile	Leu	Asp
65				70						75					80
Met	Val	Lys	Val	Met	Thr	Phe	Ala	Leu	Gln	Glu	Gly	Lys	Val	Ala	Ile
				85					90					95	
His	Cys	His	Ala	Gly	Leu	Gly	Arg	Thr	Gly	Val	Leu	Ile	Ala	Cys	Tyr
			100					105					110		
Leu	Val	Phe	Ala	Thr	Arg	Met	Thr	Ala	Asp	Gln	Ala	Ile	Ile	Phe	Val
		115					120					125			
Arg	Ala	Lys	Arg	Pro	Asn	Ser	Ile	Gln	Thr	Arg	Gly	Gln	Leu	Leu	Cys
	130					135					140				
Val	Arg	Glu	Phe	Thr	Gln	Phe	Leu	Thr	Pro	Leu	Arg	Asn	Ile	Phe	Ser
145					150					155					160
Cys	Cys	Asp	Pro	Lys	Ala	His	Ala	Val	Thr	Leu	Pro	Gln	Tyr	Leu	Ile
				165					170					175	
Arg	Gln	Arg	His	Leu	Leu	His	Gly	Tyr	Glu	Ala	Arg	Leu	Leu	Lys	His
			180					185						190	
Val	Pro	Lys	Ile	Ile	His	Leu	Val	Cys	Lys	Leu	Leu	Leu	Asp	Leu	Ala
		195					200					205			
Glu	Asn	Arg	Pro	Val	Met	Met	Lys	Asp	Val	Ser	Glu	Gly	Pro	Gly	Leu
	210					215					220				
Ser	Ala	Glu	Ile	Glu	Lys	Thr	Met	Ser	Glu	Met	Val	Thr	Met	Gln	Leu
225					230					235					240
Asp	Lys	Glu	Leu	Leu	Arg	His	Asp	Ser	Asp	Val	Ser	Asn	Pro	Pro	Asn
				245					250					255	
Pro	Thr	Ala	Val	Ala	Ala	Asp	Phe	Asp	Asn	Arg	Gly	Met	Ile	Phe	Ser
			260					265					270		
Asn	Glu	Gln	Gln	Phe	Asp	Pro	Leu	Trp	Lys	Arg	Arg	Asn	Val	Glu	Cys
		275					280					285			
Leu	Gln	Pro	Leu	Thr	His	Leu	Lys	Arg	Arg	Leu	Ser	Tyr	Ser	Asp	Ser



Val Asn Phe Asp Ser Glu Asn Gly Pro Thr Val Tyr Asn Thr Leu Lys  
 625 630 635 640

Lys Ile Phe Lys His Thr Leu Glu Glu Lys Arg Lys Met Thr Lys Asp  
 645 650 655

Gly Pro Lys Pro Gly Leu  
 660

<210> 179  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthesized Oligonucleotide.

<400> 179  
 ggauaucacu acugcauugc cugga 25

<210> 180  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthesized Oligonucleotide.

<400> 180  
 uacagcagau cugugcaggc caggu 25

<210> 181  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthesized Oligonucleotide.

<400> 181  
 ugaucacaca guagcggaag augcu 25

<210> 182  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Synthesized Oligonucleotide.

<400> 182  
 aggaguagca gaaugguuag ccuuc 25

<210> 183  
 <211> 25  
 <212> DNA

<213> Artificial

<220>

<223> Synthesized Oligonucleotide.

<400> 183  
ugaaagcagg cgagauucga uccga 25

<210> 184  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 184  
actaccgcct cacacgcttc 20

<210> 185  
<211> 20  
<212> DNA  
<213> Homo sapiens

<400> 185  
cttgactcca gcagggttc 20

<210> 186  
<211> 26  
<212> DNA  
<213> Homo sapiens

<400> 186  
atcaagtgtg acccagactg cctccg 26

<210> 187  
<211> 28  
<212> DNA  
<213> Homo sapiens

<400> 187  
catatgggat ccatggccca tgagattg 28

<210> 188  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 188  
ggtaccctcg agtcaggaga cctcaatgat 30

<210> 189  
<211> 30  
<212> DNA  
<213> Homo sapiens

<400> 189  
ggtaccctcg agtcaagtct ggttcttaat 30

<210> 190  
 <211> 664  
 <212> PRT  
 <213> Homo sapiens

<400> 190

```

Met Ala His Glu Ile Gly Thr Gln Ile Val Thr Glu Arg Leu Val Ala
1          5          10          15

Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg Pro
20        25        30

Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile Asn
35        40        45

Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu Ile
50        55        60

Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp Cys
65        70        75        80

Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala Ser
85        90        95

Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu Lys
100       105       110

Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe Ser
115       120       125

Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro Thr
130       135       140

Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr Arg
145       150       155       160

Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn Lys
165       170       175

Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser Asn
180       185       190

Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg Val
195       200       205

Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp Lys
210       215       220

Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val Leu
225       230       235       240

Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile Ala
245       250       255

Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg Phe
260       265       270

Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu Gly
  
```

275	280	285
Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Ala Gly Ala Ser		
290	295	300
Gly Pro Lys Ser Lys Leu Lys Leu Leu His Leu Glu Lys Pro Asn Glu		
305	310	315
Pro Val Pro Ala Val Ser Glu Gly Gly Gln Lys Ser Glu Thr Pro Leu		
	325	330
Ser Pro Pro Cys Ala Asp Ser Ala Thr Ser Glu Ala Ala Gly Gln Arg		
	340	345
Pro Val His Pro Ala Ser Val Pro Ser Val Pro Ser Val Gln Pro Ser		
	355	360
Leu Leu Glu Asp Ser Pro Leu Val Gln Ala Leu Ser Gly Leu His Leu		
370	375	380
Ser Ala Asp Arg Leu Glu Asp Ser Asn Lys Leu Lys Arg Ser Phe Ser		
385	390	395
Leu Asp Ile Lys Ser Val Ser Tyr Ser Ala Ser Met Ala Ala Ser Leu		
	405	410
His Gly Phe Ser Ser Ser Glu Asp Ala Leu Glu Tyr Tyr Lys Pro Ser		
	420	425
Thr Thr Leu Asp Gly Thr Asn Lys Leu Cys Gln Phe Ser Pro Val Gln		
	435	440
Glu Leu Ser Glu Gln Thr Pro Glu Thr Ser Pro Asp Lys Glu Glu Ala		
450	455	460
Ser Ile Pro Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln Ser		
465	470	475
Lys Arg Leu His Ser Val Arg Thr Ser Ser Ser Gly Thr Ala Gln Arg		
	485	490
Ser Leu Leu Ser Pro Leu His Arg Ser Gly Ser Val Glu Asp Asn Tyr		
	500	505
His Thr Ser Phe Leu Phe Gly Leu Ser Thr Ser Gln Gln His Leu Thr		
	515	520
Lys Ser Ala Gly Leu Gly Leu Lys Gly Trp His Ser Asp Ile Leu Ala		
530	535	540
Pro Gln Thr Ser Thr Pro Ser Leu Thr Ser Ser Trp Tyr Phe Ala Thr		
545	550	555
Glu Ser Ser His Phe Tyr Ser Ala Ser Ala Ile Tyr Gly Gly Ser Ala		
	565	570
Ser Tyr Ser Ala Tyr Ser Arg Ser Gln Leu Pro Thr Cys Gly Asp Gln		
	580	585
Val Tyr Ser Val Arg Arg Arg Gln Lys Pro Ser Asp Arg Ala Asp Ser		
	595	600
		605

Arg Arg Ser Trp His Glu Glu Ser Pro Phe Glu Lys Gln Phe Lys Arg  
610 615 620

Arg Ser Cys Gln Met Glu Phe Gly Glu Ser Ile Met Ser Glu Asn Arg  
625 630 635 640

Ser Arg Glu Glu Leu Gly Lys Val Gly Ser Gln Ser Ser Phe Ser Gly  
645 650 655

Ser Met Glu Ile Ile Glu Val Ser  
660

<210> 191  
<211> 302  
<212> PRT  
<213> Homo sapiens

<400> 191

Met Ala His Glu Ile Val Gly Thr Gln Ile Val Thr Glu Arg Leu Val  
1 5 10 15

Ala Leu Leu Glu Ser Gly Thr Glu Lys Val Leu Leu Ile Asp Ser Arg  
20 25 30

Pro Phe Val Glu Tyr Asn Thr Ser His Ile Leu Glu Ala Ile Asn Ile  
35 40 45

Asn Cys Ser Lys Leu Met Lys Arg Arg Leu Gln Gln Asp Lys Val Leu  
50 55 60

Ile Thr Glu Leu Ile Gln His Ser Ala Lys His Lys Val Asp Ile Asp  
65 70 75 80

Cys Ser Gln Lys Val Val Val Tyr Asp Gln Ser Ser Gln Asp Val Ala  
85 90 95

Ser Leu Ser Ser Asp Cys Phe Leu Thr Val Leu Leu Gly Lys Leu Glu  
100 105 110

Lys Ser Phe Asn Ser Val His Leu Leu Ala Gly Gly Phe Ala Glu Phe  
115 120 125

Ser Arg Cys Phe Pro Gly Leu Cys Glu Gly Lys Ser Thr Leu Val Pro  
130 135 140

Thr Cys Ile Ser Gln Pro Cys Leu Pro Val Ala Asn Ile Gly Pro Thr  
145 150 155 160

Arg Ile Leu Pro Asn Leu Tyr Leu Gly Cys Gln Arg Asp Val Leu Asn  
165 170 175

Lys Glu Leu Met Gln Gln Asn Gly Ile Gly Tyr Val Leu Asn Ala Ser  
180 185 190

Asn Thr Cys Pro Lys Pro Asp Phe Ile Pro Glu Ser His Phe Leu Arg  
195 200 205

Val Pro Val Asn Asp Ser Phe Cys Glu Lys Ile Leu Pro Trp Leu Asp  
210 215 220

Lys Ser Val Asp Phe Ile Glu Lys Ala Lys Ala Ser Asn Gly Cys Val  
 225 230 235 240

Leu Val His Cys Leu Ala Gly Ile Ser Arg Ser Ala Thr Ile Ala Ile  
 245 250 255

Ala Tyr Ile Met Lys Arg Met Asp Met Ser Leu Asp Glu Ala Tyr Arg  
 260 265 270

Phe Val Lys Glu Lys Arg Pro Thr Ile Ser Pro Ser Phe Asn Phe Leu  
 275 280 285

Gly Gln Leu Leu Asp Tyr Glu Lys Lys Ile Lys Asn Gln Thr  
 290 295 300

<210> 192  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 192

Lys Asn Gln Thr Gly Ala Ser Gly Pro Lys Ser Lys Lys Leu Lys Leu  
 1 5 10 15

Leu His Leu Glu  
 20

<210> 193  
 <211> 19  
 <212> PRT  
 <213> artificial

<220>  
 <223> Synthesized Oligonucleotide.

<400> 193

Cys Lys Lys Leu Gln Thr Ala Arg Pro Ser Asp Ser Gln Ser Lys Arg  
 1 5 10 15

Leu His Ser

<210> 194  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
 ctgcgtgttg cactgcatag t

21

<210> 195  
 <211> 19  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 tgggcaagga aagcttcct

19



26

21

23

23

23

20

---

---

---

---

---

25

25

25

27

27

25

25

<400> 206

Val Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Lys  
115 120 125

Glu Glu Lys Glu Met Ile Phe Glu Asp Thr Asn Leu Lys Leu Thr Leu  
 130 135 140  
 Ile Ser Glu Asp Ile Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu  
 145 150 155 160  
 Glu Asn Leu Thr Thr Gln Glu Thr Arg Glu Ile Leu His Phe His Tyr  
 165 170 175  
 Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu  
 180 185 190  
 Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Pro Glu His  
 195 200 205  
 Gly Pro Val Val Val His Ser Ser Ala Gly Ile Gly Arg Ser Gly Thr  
 210 215 220  
 Phe Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp  
 225 230 235 240  
 Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Lys Phe  
 245 250 255  
 Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu  
 260 265 270  
 Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln  
 275 280 285  
 Asp Gln Trp Lys Glu Leu Ser His Glu Asp Leu Glu Pro Pro Pro Gly  
 290 295 300  
 His Ile Pro Pro Pro Pro Arg Pro Pro Lys Arg Ile Leu Glu Pro His  
 305 310 315 320

Asn

<210> 207  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 207

Ser Gly Ser Phe Glu Leu Ser Val Gln Asp Leu Asn Asp Leu Leu Ser  
 1 5 10 15  
 Asp Gly Ser Gly Cys Tyr Ser Leu Pro Ser Gln Pro Cys Asn Glu Val  
 20 25 30  
 Thr Pro Arg Ile Tyr Val Gly Asn Ala Ser Val Ala Gln Asp Ile Pro  
 35 40 45  
 Lys Leu Gln Lys Leu Gly Ile Thr His Val Leu Asn Ala Ala Glu Gly  
 50 55 60  
 Arg Ser Phe Met His Val Asn Thr Asn Ala Asn Phe Tyr Lys Asp Ser  
 65 70 75 80

Gly Ile Thr Tyr Leu Gly Ile Lys Ala Asn Asp Thr Gln Glu Phe Asn  
85 90 95

Leu Ser Ala Tyr Phe Glu Arg Ala Ala Asp Phe Ile Asp Gln Ala Leu  
100 105 110

Ala Gln Lys Asn Gly Arg Val Leu Val His Cys Arg Glu Gly Tyr Ser  
115 120 125

Arg Ser Pro Thr Leu Val Ile Ala Tyr Leu Met Met Arg Gln Lys Met  
130 135 140

Asp Val Lys Ser Ala Leu Ser Ile Val Arg Gln Asn Arg Glu Ile Gly  
145 150 155 160

Pro Asn Asp Gly Phe Leu Ala Gln Leu Cys Gln Leu Asn Asp Arg Leu  
165 170 175

Ala Lys Glu Gly Lys Leu Lys Pro  
180

<210> 208  
<211> 144  
<212> PRT  
<213> Homo sapiens

<400> 208

Ala Ser Phe Pro Val Glu Ile Leu Pro Phe Leu Tyr Leu Gly Cys Ala  
1 5 10 15

Lys Asp Ser Thr Asn Leu Asp Val Leu Glu Glu Phe Gly Ile Lys Tyr  
20 25 30

Ile Leu Asn Val Thr Pro Asn Leu Pro Asn Leu Phe Glu Asn Ala Gly  
35 40 45

Glu Phe Lys Tyr Lys Gln Ile Pro Ile Ser Asp His Trp Ser Gln Asn  
50 55 60

Leu Ser Gln Phe Phe Pro Glu Ala Ile Ser Phe Ile Asp Glu Ala Arg  
65 70 75 80

Gly Lys Asn Cys Gly Val Leu Val His Ser Leu Ala Gly Ile Ser Arg  
85 90 95

Ser Val Thr Val Thr Val Ala Tyr Leu Met Gln Lys Leu Asn Leu Ser  
100 105 110

Met Asn Asp Ala Tyr Asp Ile Val Lys Met Lys Lys Ser Asn Ile Ser  
115 120 125

Pro Asn Phe Asn Phe Met Gly Gln Leu Leu Asp Phe Glu Arg Thr Leu  
130 135 140